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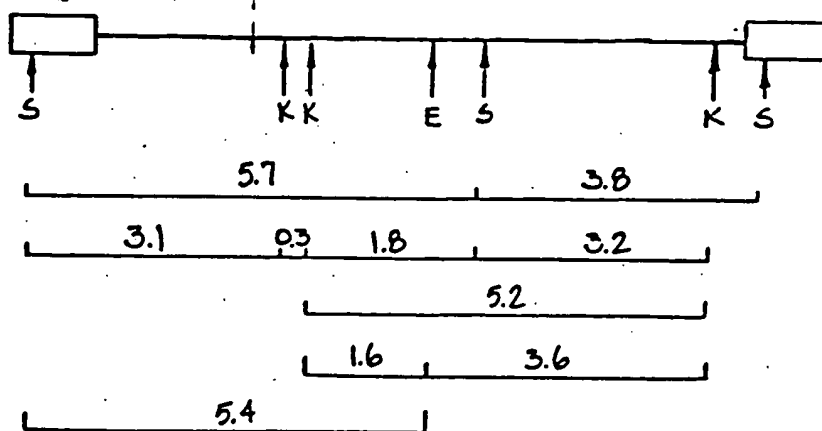


FIG. 1.

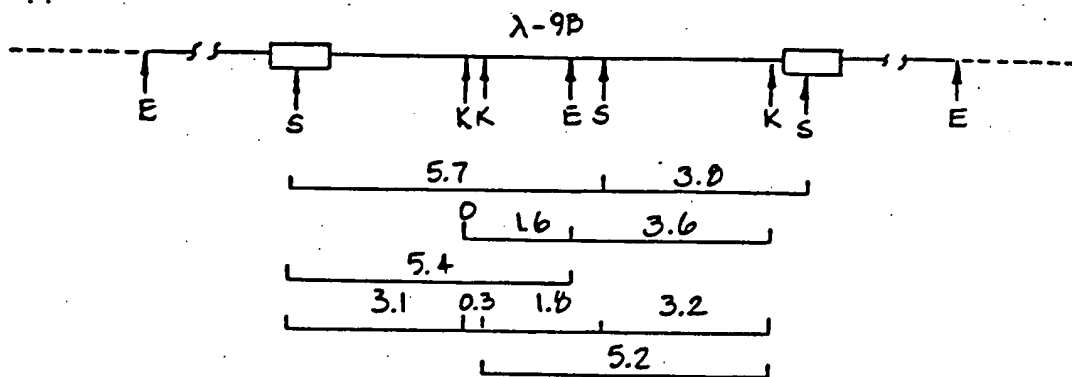


FIG. 2.

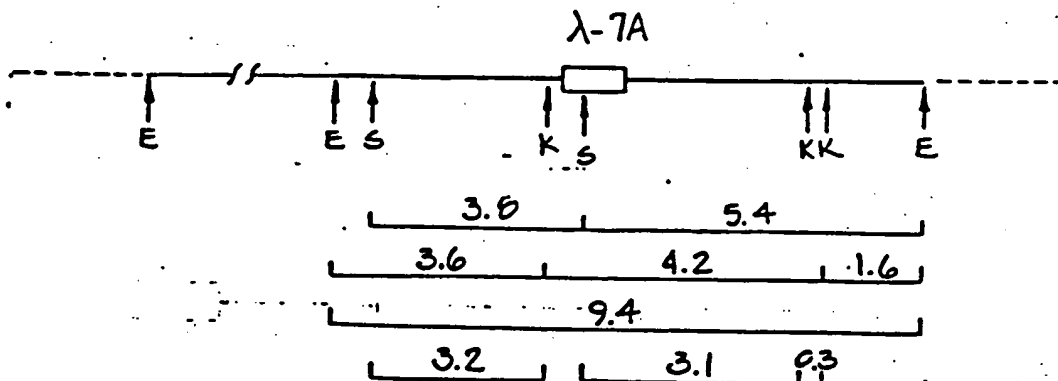


FIG. 3.

Handwritten signature or initials.

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On Oct 24 14:16:11 1984

Argument Map in DNA Strand ssarv2
from the '/v/lib/6mers' file.
Translation shown at open reading frames.

FIGURE 4
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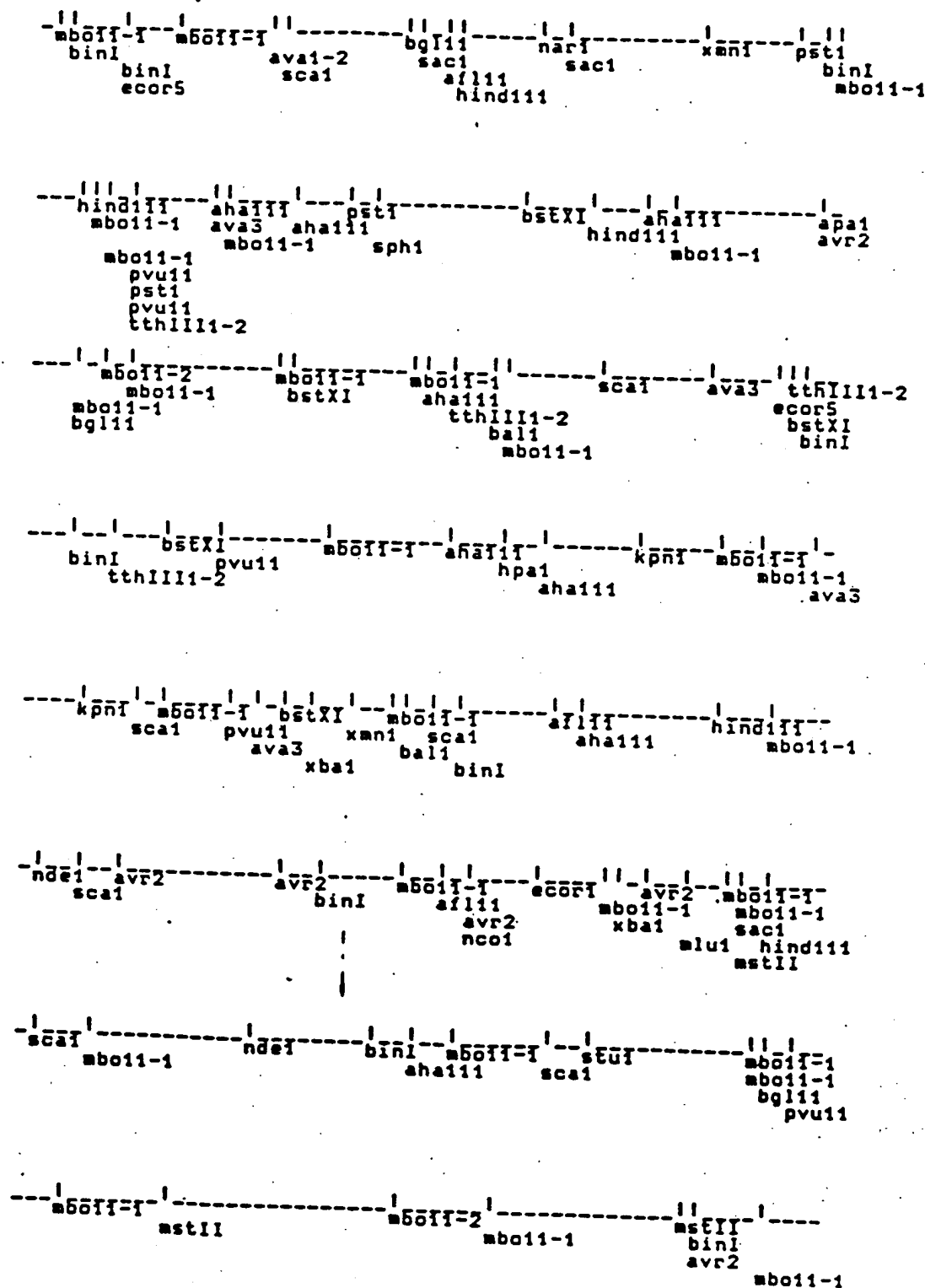
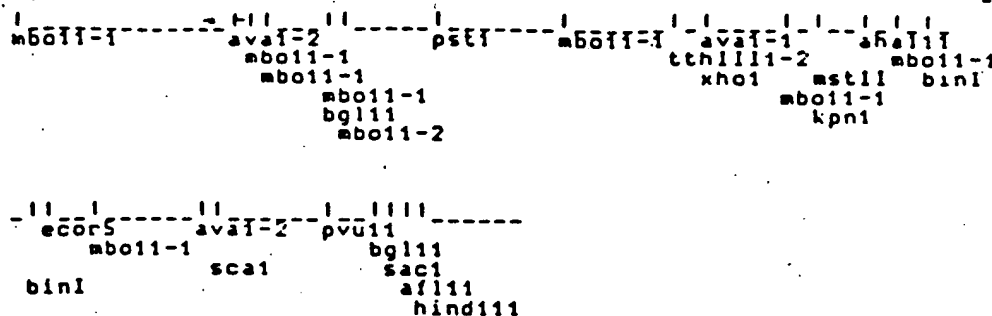


Figure 4
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1 CTGGAAGGGCTAATTTGGTCCCAAGAGACAAGAGATCCTTGATCTGTGGATCTACCACAC
 63 GACCTTCCCATTAAACCAGGGTTCTTCTGTTCTCTAGGAACCTAGACACCTAGATGGTGTG
 123 26 mbo11, 50 bnl1,
 183 ACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACT
 243 TGTTCCGATGAAGGGACTAACCCTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGA
 303 107 bnl1, 113 ecor5,
 363 GACCTTTGGATGGTGTCTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAA
 423 CTGGAACCTACCACGAAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTT
 483 172 mbo11,
 543 TGAAGGAGAGAACAACAGCTTGTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGA
 603 ACTTCTCTCTTGTGTGCAACAATGTGGGATACTCGGACGTACCCTACCTCTGCGCT
 663 296 ava1,
 723 GCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGC
 783 CGACGTAGGCCTCATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCG
 314 sca1,
 363 TGGGGACTTTCCAGGGAGGCGTGGCCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGC
 423 ACCCTGAAAGGTCCCTCCGACCGGACCGCCCTGACCCCTCACCAGGGAGTCTACG
 483 TGCATATAAGCAGACTGCTTTTTGCTGTACTGGGTCTCTCTGTTAGACCAGATCTGAG
 543 ACGTATATTCGTCTGACGAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTC
 603 474 bgl11,
 663 CCTGGGAGCTCTCTGGCTAACTAGGGAAACCACTGCTTAAGCCTCAATAAGCTTGCCTT
 723 GGACCCTCGAGAGACCGATTGATCCCTTGGGTGACGAATTCGGAGTTATTTGAAACGGAA
 783 488 sac1, 518 afl11, 532 hind111,
 363 GAGTGTCTCAAGTAGTGTGTGCCCCTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCA
 423 CTCACGAAGTTCATCACACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGT
 483 639 nar1,
 543 CGAAAGTAGAACCAGAGGAGCTCTCTCGACGAGGACTCGGCTTGTGAAGCGGCGACAG
 603 GCTTTTATCTTGGTCTCTCGAGAGAGCTGCTCTGAGCCGAACGACTTCGCGCTGTG
 663 680 sac1,
 723 CAAGAGGCGAGGGGCGGCGACTGGTGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAG
 783 GTTCTCCGCTCCCGCCGCTGACCACTCATGCGTTAAAACTGATCGCCTCCGATCTTC
 MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspLysTrpGlu
 GAGAGAGAGATGGGTGCGAGAGCGTCCGTATTAAGCGGGGGAGAATTAGATAAATGGGAA
 CTCTCTCTACCCACGCTCTCGAGCCATAATTCGCCCCCTCTTAATCTATTTACCTT

843 LysIleArgLeuArgProGlyGlyLysLysTyrLysLeuLysHisIleValTrpAla
AAAATTTCGGTTAAGGCCAGGGGGGAAAGAAAAATATAAGTTAAACATATAGTATGGCA
TTTTAAGCCAATTCCGGTCCCCCTTTCTTTTTATATTCAATTTGTATATCATACCCGT

903 SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
AGCAGGGAGCTAGAACGATTCCGAGTCAATCCTGGCCTGTTAGAAACATCAGAAGGCTGC
TCGTCCCTCGATCTTGCTAAGCGTCAGTTAGGACGGACAATCTTTGTAGTCTTCCGACG

959 pst1,

963 ArgGlnIleLeuGlyGlnLeuGlnProSerLeuGlnThrGlySerGluGluLeuArgSer
AGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAAGAACTTAGATCA
TCTGTTTATAACCTGTGATGTGCGTAGGGAAGTCTGTCTAGTCTTCTTGAATCTAGT

1002 bin1, 1008 mbo11,

1023 LeuTyrAsnThrValAlaThrLeuTyrCysValHisGlnArgIleAspValLysAspThr
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AATATATTATGTCATCGTTGGGAGATAACACATGTAGTTCTCTATCTACATTTTCTGTGG

1083 LysGluAlaLeuGluLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGln
AAGGAAGCTTTAGAGAAAGATAGAGGAAGAGCAAAACAAAGTAAGAAAAAGGCACAGCAA
TTCCTTCGAAATCTCTTCTATCTCTCTCTGTTTTGTTTTATTCTTTTTCCGTGCGT

1087 hind111, 1097 mbo11, 1107 mbo11,

p25

1143 AlaAlaAlaAlaAlaGlyThrGlyAsnSerSerGlnValSerGlnAsnTyrProIleVal
GCAGCAGCTGCAGCTGGCACAGGAACAGCAGCCAGGTGAGCCAAATACCTATAGTG
CGTCTGACGCTGACCGTGTCTTTGTCTGCTGCGTGGTTCAGTGGTTTTAATGGGATATCAC

1147 pvu11, 1150 pst1, 1153 pvu11, 1156 tthIII1,

1203 GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
CAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAAGTTAAATGCATGG
GTCTTGGATGTCCCCGTTTACCATGTAGTCCGGTATAGTGGATCTTGAAATTTACGTACC

1250 aha111, 1255 ava3,

1263 ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
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CATTTTCATCATCTTCTTTTCCGAAAGTGGGTCTTCATTATGGGTACAAAAGTCGTAAT

1275 mbo11,

1323 SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
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AGTCTTCCTCGGTGGGTGTTCTAAATTTGTGGTACGATTTGTGTACCCCCCTGTAGTT

1346 aha111,

1383 AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal
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CGTCGGTACGTTTACAATTTTCTCTGATAGTTACTCTTCGACGCTTACCCTATCTCAC

1423 pst1,

1443 HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp
CATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGGGGAAGTGAC
GTAGGTCACTGACGTCCCGGATAACGTGGTCCGGTTTACTCTCTTGGTTCCCCTTCACTG

1451 sph1,

1503 IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro
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TATCCTCTTGTATGATCATGGGAAGTCTTGTATTATCTTACCTACTGTTTATTAGGTGGA

1563 IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg
ATCCAGTAGGAGAAATCTATAAAGATGGATAATCCTGGGATTAATAATAATAGTAAGA
TAGGGTCATCTCTTTAGATATTTTCTACCTATTAGGACCCCTAATTTTATCATTCT

1623 MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp
ATGTATAGCCCTACAGCATTCTGGACATAAGACAAGGACCAAGGAACCTTTAGAGAT
TACATATCGGGAATGCTGTAAGACCTGTATTCTGTTCTGTTCTTGGGAAATCTCTA

1636 bstXI,

1683 TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn
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ATACATCTGGCCAAGATATTTTGAGATTCTCGGCTTGTTCGAAGTGTCTACATTTTTA

1720 hind111,

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Figure 4
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1743 TrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys
TGGATGACAGAAACCTTGTGGTCCAAAATGCAAAACCCAGATTGTAAGACTATTTTAAAA
ACCTACTGTCTTTGGAACAACCAGGTTTTACGTTTGGGTCTAACATTCTGATAAAATTTT
1796 sha111,

1803 AlaLeuGlyProAlaAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGly
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CGTAACCTGGTCGTGATGTGATCTTCTTTACTACTGTCTACAGTCCCTCACCCCCCT
1827 mbo11,

1863 ProGlyHisLysAlaArgValLeuAlaGluAlaMetSerGlnValThrAsnProAlaAsn
CCCGGCCATAAAGCAAGAGTTTTGGCTGAAGCCATGAGCCAAGTAACAAATCCAGCTAAC
GGGCCGCTATTTCGTTCTCAAAACCGACTTCGGTACTCGGTTTCATTGTTTAGGTCGATTG
p18

1923 IleMetMetGlnArgGlyAsnPheArgAsnGlnArgLysThrValLysCysPheAsnCys
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TATTACTACGTCTCTCCGTTAAATCCTTGGTTTTCTTTCTGACAATTCACAAAGTTAACA

1983 GlyLysGluGlyHisIleAlaLysAsnGlyArgAlaProArgLysLysGlyCysTrpArg
GGCAAAAGAAAGGACACATAGCCAAATTCAGGGGCCCTAGGAAAAAGGGCTGTTGGAGA
CCGTTTCTTCCCCTGTATCGGTTTTTAACGTCCCGGGGATCCTTTTTCCCGACAACCTCT
2014 apa1, 2019 avr2,

2043 CysGlyArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGly
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ACACCTTCCCTTCTGTGGTTTACTTTCTAACGTGACTCTCTGTCCGATTAAAAATCCC
2102 mbo11,

2103 LysIleTrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluPro
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TTCTAGACCAGGAAGGATGTTCCCTTCCGGTCCCTTAAAGAAAGTCTCGTCTGGTCTCGGT
2104 bgl11, 2141 mbo11,

2163 ThrAlaProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLys
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TGTCCGGGTGGTCTTCTCTCGAAGTCAAACCCCTCCTCTTTTGTGAGGGAGAGTCTTC
2175 mbo11,

2223 GlnGluProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsn
CAGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAAC
GTCTCCTCGGCTATCTGTTCTTGACATAGGAAATTGAAGGGAGTCTAGTGAGAAACCGTTG

2283 AspProSerSerGlnOC
GACCCCTCGTCACAATAAGGATAGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGA
CTGGGGAGCAGTGTTATTCTATCCCCCGTTGATTCTTCGAGATAATCTATGTCTT

2342 MetAsnLeuProGlyLysTrpLysProLysMetIle
GCAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAATGGAAACCAAAATGATA
CGTCTACTATGTCATAATCTTCTTTACTTAAACGGTCTTTTACCTTTGGTTTTTACTAT
2360 mbo11, 2375 bstX1,

2402 GlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGlnIleProValGluIleCys
GGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTACGATCAGATACCTGTAGAAATCTGT
CCCCCTTAACCTCCAAAATAGTTTCATTCTGTCTAGTCTATGGACATCTTTAGACA

2462 GlyHisLysAlaIleGlyThrValLeuValGlyProThrProValAsnIleIleGlyArg
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CTGTATTTTCGATATCCATGTCATAATCATCCTGGATGTGGACAGTTGTATTAACTTCT
2517 mbo11,

2522 AsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrVal
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TTAGACAACCTGAGTCTAACCAACATGAAATTTAAAGGGGTAATCAGGATAACTTTGACAT
2548 sha111, 2577 tth1111,

2582 ProValLysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeuThrGlu
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GGTCATTTTAATTTCCGTCTTACCTACC66GTTTTCAATTCGTTACCGGTAACCTGTCTT
2627 bal1, 2639 mbo11,

2642 GluLysIleLysAlaLeuValGluIleCysThrGluMetGluLysGluGlyLysIleSer
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CTTTTTTATTTTCTAATCATCTCTATACATGTCTTTACCTTTTCTTCCCTTTAAAGT

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Figure 4
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2702 LysIleGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSer
AAAATTGGGCCTGAAAATCCATACAACTACTCCAGTATTTGCTATAAAGAAAAAGACAGT
TTTAAACCCGGACTTTTAGGTATGTTATGAGGTCATAAACGATATTTCTTTTTCTGTCA
2759 sca1,
2762 ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp
ACTAAATGGAGAAAAGTAGTAGATTTTACAGAGAACTTAATAAAGAACTCAAGACTTCTGG
TGATTTACCTCTTTTGATCATCTAAAGTCTCTTGAATTATTTTCTTGAGTTCTGAAGACC
2822 GluValGlnLeuGlyIleProHisProGlnGlyOC
GAAGTTCAGTTAGGAATACCAACCCCGCAGGGTTAAAAAAGAAAAATCAGTAACAGTA
CTTCAAGTCAATCCTTATGGTGTGGGCGTCCCAATTTTTTCTTTTTTAGTCATTGTCTAT
2882 TTGGATGTGGGTGATGCATCTTTTTCAGTTCCTTAGATAAAGACTTTAGAAAGTATACTG
AACCTACACCCACTACGTATGAAAAGTCAAGGGAATCTATTTCTGAAATCTTTCATATGAC
2895 ava3,
2943 CATTTACCATACCTAGTATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGG
GTAAATGGTATGGATCATATTTGTTACTCTGTGGTCCCTAATCTATAGTCATGTTACACC
2985 ecor5,
3003 LeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeu
CTGCCACAGGGATGGAAAGGATCACCAGCAATATTCAAAGTAGCATGACAAAAATCTTA
GACGGTGTCCCTACCTTTCTAGTGGTCTGTATAAGGTTTCATCGTACTGTTTTAGAAAT
3003 tthIII1, 3006 bstXI, 3021 binI,
3063 GluProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr
GAGCCTTTTAGAAAACAGAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTAT
CTCGGAAAAATCTTTTGTCTTAGGTCGTATCAATAGATAGTTATGTACCTACTAAACATA
3123 ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHis
GTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAAAAATAGAGGAAGTGAAGACAGCAT
CATCTAGACTGAATCTTTATCCCGTCGTATCTTGTTTTTATCTCCTTGACTCTGTCTGA
3126 binI, 3171 tthIII1,
3183 LeuLeuArgTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeu
CTGTTGAGGTGGGGATTTACCACACCAGACAAAAACATCAGAAAGAACCTCCATTCCTT
GCAACTCCACCCCTAAATGGTGTGGTCTGTTTTTTGTAGTCTTTCTTGGAGGTAAGGAA
3234 bstXI,
3243 TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGlu
TGGATGGGTTATGAATCCATCCTGATAAATGACAGTACAGCCTATAATGCTGCCAGAA
ACCTACCCAATACCTGAGGTAGGACTATTTACCTGTCTGTCGATATTACGACGGTCTT
3303 LysAspSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer
AAAGACAGCTGACTGTCAATGACATACAGAAGTTAGTGGGAAAAATTGAATTGGGCAAGT
TTTCTGTCGACCTGACAGTTACTGTATGTCTTCAATCACCTTTTAACCTAACCCGTTCA
3308 pvu11,
3363 GlnIleTyrAlaGlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyThrLysAla
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GTCTAAATACGTCCCTAATTTTCAATTCGTCAATACATTTGAGGAATCTCCTTGGTTTCGT
3423 LeuThrGluValIleProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGlu
CTAACAGAAAGTAATACCACTAACAGATGAGGAGCAGAGCTAGAACTGGCAGAAAAACAGGGAG
GATTGTCTTCATTATGGTGTGTTCTTCTTCTCGATCTTGACCGTCTTTTGTCCCTC
3447 abo11,
3483 IleLeuLysGluProValHisGluValTyrTyrAspProSerLysAspLeuValAlaGlu
ATTCTAAAAGAACAGTACATGAAGTATATTATGACCATCAAAAGACTTAGTACAGAA
TAAGATTTTCTTGGTCATGTACTTCAATAATACTGGGTAGTTTTCTGAATCATCGTCTT
3543 IleGlnLysGlnGlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsn
ATACAGAAGCAGGGCAAGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAAT
TATGTCTTCTGTCCTCCGTTACCTGTATAGTTTAAATAGTTCTCGGTAATTTTTTA
3594 sha111,
3603 LeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeu
CTGAAAACAGGAAAGTATGCAAGGATGAGGGGTGCCACACTAATGATGTAAAACAGTTA
GACTTTTGTCTTTCATACGTTCTACTCCCAAGGGGTGATGATTACTACATTTTGTCAAT
3659 hpa1,

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3663 ThrGluAlaValGlnLysValSerThrGluSerIleValIleTrpGlyLysIleProLys
ACAGAGGCAGTGCAGAAAGTATCCACAGAAAGCATAGTAATATGGGGAAAGATTCTTAA
TGTCCTCCGTACGTTTTTCATAGGTGTCTTTCGTATCATTATACCCCTTCTAAGGATT

3723 PheLysLeuProIleGlnLysGluThrTrpGluAlaTrpTrpMetGluTyrTrpGlnAla
TTTAAACTACCCATACAAAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCT
AAATTTGATGGGTATGTTTCTCTTGTACCCTTCGTACCACCTACCTCATAACCGTTCGA
3723 sha111,

3783 ThrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGln
ACCTGGATTCTGAGTGGGAGTTTGTCAATACCCCTCCCTTAGTGAAATTATGGTACCAG
TGGACCTAAGGACTCACCTCAAACAATTATGGGGAGGGAATCACTTTAATACCATGGTC
3835 kpn1,

3843 LeuGluLysGluProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArg
TTAGAGAAAGAACCATAGTAGGAGCAGAACTTTCTATGTAGATGGGGCAGCTAATAGG
AATCTCTTTCTTGGGTATCATCTCTGTCTTGGAAAGATACATCTACCCCGTCGATTATCC

3903 GluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSer
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CTCTGATTTAATCCTTTTCTCTATACAATGACTGTCTCTCTGTTTTTCAACAGAGG
3943 mbo11,

3963 IleAlaAspThrThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAsp
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TATCGACTGTGTTGTTTAGTCTTCTGACTTAATGTTCTGTTAAGTAGATCGAAACGTCCTA
3983 mbo11,

4023 SerGlyLeuGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAla
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AGCCCTAATCTTCATTTGTATCATTGTCTGAGTGTTATACGTAATCCTTAGTAAGTTCGT
4060 ava3,

4083 GlnProAspLysSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLysLys
CAACGAGATAAGAGTGAATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAG
GTTGGTCTATTCTCACTTAGTCTCAATCAGTCAGTTTATTATCTCGTCAATTATTTTTTC

4143 GluLysValTyrLeuAlaTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnVal
GAAAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTA
CTTTTCCAGATGGACCGTACCCATGGTCTGTGTTTCTTAACCTCCTTTACTTGTTCAT
4163 kpn1,

4203 AspLysLeuValSerAlaGlyIleArgLysValLeuPheLeuAsnGlyIleAspLysAla
GATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTTTGAATGGAATAGATAAGGCC
CTATTTAATCAGTCACGACCTTAGTCCTTTCATGATAAAAACTTACCTTATCTATTCCGG
4232 sca1,

4263 GlnGluGluHisGluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeu
CAAGAAGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTG
GTTCTTCTGTACTCTTTATAGTGTCTTAACCTCTCGTTACCGATCACTAAAATTGGAC
4266 mbo11,

4323 ProProValValAlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGlu
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GGTGGACATCATCGTTTTCTTTATCATCGGTGACACTATTTACAGTCGATTTTCTCTT
4352 pvu11,

4383 AlaMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeu
GCCATGCATGGACAAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTA
CGGTACGTACCTGTTTCATCTGACATCAAGTCTTATACCGTTGATCTAACATGTGTAGAT
4386 ava3, 4410 bstXI, 4439 xba1,

4443 GluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIleGluAlaGluVal
GAAGGAAAAATTATCCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTT
CTTCTTTTTTAAGGACCATCGTCAAGTACATCGGTACCTATATATCTTCGTCTTCAA
4497 xmn1,

4503 IleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeuAlaGlyArgTrp
ATTCCAGCAGAGACAGGACAGGAAACAGCATATTTTCTCTTAAATAGCAGGAAGATGG
TAAGGTCGTCTCTGTCCCGTCTTTGTCTGTATAAAAGAGAATTTTAATCGTCTTCTACC
4555 mbo11, 4560 bal1,

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4563 ProValLysThrIleHfsThrAspAsnGlySerAsnPheThrSerThrThrValLysAla
CCAGTAAAAACAATACATACAGACAATGGCAGCAATTTCCACAGTACTACGGTTAAGGCC
GGTCATTTTTTGTATGTATGTCTGTTACCGTCGTTAAAGTGGTCATGATGCCAATTCGGG

4605 sca1,

4623 AlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGln
GCCTGTTGGTGGGCAGGGATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAGTCAA
CGGACAACCACCCGTCCTAGTTCGTCCTTAAACCGTAAGGGATGTTAGGGGTTTCAGTT

4639 bin1,

4683 GlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGln
GGAGTAGTAGAATCTATGAATAATGAATTAAGAAAATTATAGGACAGGTAAGAGATCAG
CCTCATCATCTTAGATACTTATTACTTAATTTCTTTTAATATCCTGTCCATTCTCTAGTC

4743 AlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLys
GCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTTCATCCACAATTTTAAAGAAAA
CGACTTGTGGAATTCGTGTCATGTTACCCTCATAGTAGGTGTTAAATTTTCTTTT

4752 af111, 4791 sha111,

4803 GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIle
GGGGGGATTGGGGATACAGTGCAGGGGAAAGAAATAGTAGACATAATAGCAACAGACATA
CCCCCTAACCCCTATGTCACGTCCTCTTCTTATCATCTGTATTATCGTTGTCGTAT

4863 GlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArg
CAAATAAAGAACTACAAAAGCAAATTACAAAATTCAAATTTTTCGGGTTTATTACAGG
GTTTGATTTCTTGATGTTTTTCGTTTAATGTTTTTAAGTTTTTAAAGGCCAAATAATGTCC

4923 AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAla
GACAACAAAGATCCCTTTGSAAGGACCAAGCTTCTCTGGAAGGTGAAGGGGCA
CTGTTGTTTCTAGGGGAAACCTTTCCTGTCGTTTCGAAGAGACCTTTCACCTTCCCCGT

4956 hind111,

4983 ValValIleGlnAspAsnSerAspIleLysValValProArgArgLysAlaLysIleIle
GTAGTAATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAATCATT
CATCATTATGTTCTATTATCACTGTATTTTCATCACGGTTCTTCTTTTCGTTTTTAGTAA

5023 mbo11,

5043 MetGluAsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIle
ArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArgGlnAspGluAsp
AGGGATTATGGAAAACAGATGGCAGGTGATGTTGTTGTTGCAAGTAGACAGGATGAGGAT
TCCCTAATACCTTTTGTCTACCGTCCACTACTAACACACCGTTTCATCTGTCCTACTCCTA

5103 ArgTreTrpLysSerLeuValLysHisHisMetTyrIleSerLysLysAlaLysGlyTrp
AM
TAGAACATGGAAAAGTTTAGTAAAAACCATATGTATATTTCAAAGAAAAGCTAAAAGGATGG
ATCTGTGACCTTTTCAAATCATTTTGTGGTATACATATAAAGTTTCTTTTCGATTTCCCTACC

5131 nde1,

5163 PheTyrArgHisHisTyrGluSerThrHisProArgValSerSerGluValHisIle
TTTTATAGACATCACTATGAAAGTACTCATCCAAGAGTAAGTTTCAAGAGTACACATC
AAAAATATCTGTAGTGATACTTTCATGAGTAGGTTCTCATTCAAGTCTTCATGTGTAG

5185 sca1,

5221 ProLeuGlyAspAlaLysLeuValIleThrThrTyrTrpGlyLeuHisThrGlyGluArg
CCCCTAGGGGATGCTAAATTGGTAATAACAACATATTGGGGTCTGCATACAGGAGAAAGA
GGGGATCCCCTACGATTTAACCATTATTGTTGTATAACCCCAAGACGTATGTCCTCTTTCT

5223 avr2,

5281 GluTrpHisLeuGlyGlnGlyValAlaIleGluTrpArgLysLysLysTyrSerThrGln
GAATGGCATTGTTGGCCAGGGAGTCGCCATAGAATGGAGGAAAAAGAAATATAGCACACAA
CTTACCCTAAACCCGGTCCCTCAGCGGTATCTTACCTCCTTTTTCTTTATATCCTGTGTT

5341 ValAspProGlyLeuAlaAspGlnLeuIleHisLeuHisTyrPheAspCysPheSerGlu
GTAGACCTTGGCTAGCAGACCAACTAATCATCTGCATTATTTTGTGTTTTCAGAA
CATCTGGGACCGGATCGTCTGTTGATTAAAGTAGACGTAATAAACTAACAAAAAGTCTT

5401 SerAlaIleLysAsnAlaIleLeuGlyTyrArgValSerProArgCysGluTyrGlnAla
TCTGCTATAAAAAATGCCATATTAGGATATAGAGTTAGTCCTAGGTGTGAATATCAAGCA
AGACGATATTTTTTACGGTATAATCCTATATCTCAATCAAGATCCACACTTATAGTTCGT

5440 avr2,

5461 GlyHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuAlaAlaLeuIleThrProLys
GGACATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAA
CCTGTATTGTTCCATCCTAGAGATGTTATGAACCGTGATCGTCGTAATTATTGTGGTTT

5476 bin1,

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5521 LysThrLysProProLeuProSerValLysLysLeuThrGluAspArgTrpAsnLysPro
 AAGACAAAGCCACCTTTGCCTAGTGTAAAGAACTGACAGAGGATAGATGGAACAAGCCC
 TTCTGTTTCGGTGGAACCGATCACAATTCTTTGACTGTCTCCTATCTACCTTGTTCGGG
 5581 GlnLysThrLysGlyHisArgGlySerHisThrMetAsnGlyHisAM
 CAGAAGACCAAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAGAGCTTTTAGAGG
 GTCTTCTGGTTCCGGTGTCTCCCTCGGTATGTTACTTACCTGTGATCTCGAAAATCTCC
 5583 mbo11,
 5641 AGCTTAAGAGAGAAGCTGTTAGACATTTTCTAGGCCATGGCTCCATAGCTTAGGACAAT
 TCGAATTCTCTTTCGACAATCTGTAAAAGGATCCGGTACCGAGGTATCGAATCCTGTTA
 5643 af111, 5670 avr2, 5676 nco1,
 5701 ATATCTATGAAACTTATGGGGATACCTTGGGCGAGGAGTGGAAAGCCATAATAAGAATTCTGC
 TATAGATACTTTGAATACCCCTATGAACCCGCTCTCACCTTCGGTATTATTCTTAAGACG
 5752 ecor1,
 5761 AACAACTGCTGTTTATTCATTTTCTAGAATTGGGTGTCAACATAGCAGAATAGGCATTATTC
 TTGTTGACGACAAATAAGTAAAGTCTTAACCCACAGTTGTATCGTCTTATCCGTAATAAG
 5821 AACAGAGGAGAGCAAGAAGAAATGGAAGCAGTAGATCCTAATCTAGAGCCCTGGAAGCAT
 TTGTCTCCTCTCGTTCTTCTTTACCTCGGTCTATAGGATTAGATCTCGGGACCTTCGTA
 5836 mbo11, 5862 xba1,
 5881 CCAGGAAGTCAGCCTAGGACTGCTTGTAAACAATTGCTATTGTAAAAAGTGTTCCTTCAT
 GGTCTTCAGTCGGATCCTGACGAACATTGTTAACGATAACATTTTTCACAAACGAAAGTA
 5893 avr2,
 5941 TGCTACGCGTGTTCACAAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGA
 ACGATGCGCACAAAGTGTTCCTTTCCGAATCCGTAGAGGATACCGTCTTCTTCGCTCT
 5945 mlu1, 5988 mbo11,
 6001 CAGCGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAA
 GTCGCTGCTTCTCGAGGAGTCTGTGAGTCTGAGTAGTTCGAAGAGATAGTTTCGTCATT
 6008 mbo11, 6011 sac1, 6016 mstII, 6038 hind111,
 6061 GTAGTAAATGTAATGCAATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGCA
 CATCATTTACATTACGTTAGAAATGTTTATAATCGTTATCATAGTAATCATCATCATCGT
 6121 ATAATAGCAATAGTTGTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAA
 TATTATCGTTATCAACACACCTGGTATCATGAGTATCTTATATCCTTTTATAATTCTGTT
 6147 sca1,
 6181 AGAAAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAA MetLys
 TCTTTTATCTGTCTAATTAACATCTTATTCTCTTTTTCGTCTTCTGTCAACGTTACTTT ENV
 6222 mbo11,
 6241 ValLysGlyThrArgArgAsnTyrGlnHisLeuTrpArgTrpGlyThrLeuLeuLeuGly
 GTGAAGGGGACAGGAGGAATTATCAGCACTTGTGGAGATGGGGCACCTTGCTCCTTGGG
 CACTTCCCTGGTCTCTTAATAGTCGTGAACACCTCTACCCCGTGGAAACGAGGAACCC
 6301 MetLeuMetIleCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValPro
 ATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTACAGTTTATTATGGAGTACCT
 TACAACCTACTAGACATCAGGATGTCTTTTAAACACCCAGTGTCAAATAATACCTCATGGA
 6361 ValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThr
 GTGTGGAAGAAGCAACTACCACTCTATTTTGTGCATCAGATGCTAGAGCATATGATACA
 CACACCTTTCTTCGTTGATGGTGAGATAAAACACGTAAGTCTACGATCTCGTATACTATGT
 6410 nde1,
 6421 GluValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGlu
 GAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACCCCAACCCACAAGAA
 CTCCATGTATTACAAACCCGGTGTGTACGGACACATGGGTGTCTGGGGTTGGGTGTTCTT
 6481 ValValLeuGlyAsnValThrGluAspPheAsnMetTrpLysAsnAsnMetValGluGln
 GTAGTATTGGGAAATGTGACAGAAAAATTTAACATGTGGAAAAATAACATGGTAGAACAG
 CATCATAAACCTTACACTGTCTTTTAAATTTGTACACCTTTTATTGTACCATCTTGTCT
 6541 MetGlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThr
 ATGCAGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAATTAACC
 TACGTCTCTATATTAGTCAAATACCCCTAGTTTGGGATTTCCGGTACACATTTTAATTGG
 6567 bni1,

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5601 ProLeuCysValThrLeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSer
CCACTCTGTGTTACTTTAAATTGCACTGATTTGGGGAAAGGCTACTAATACCAATAGTAGT
GGTGAGACACAATGAAATTTAACGTGACTAAACCCCTTCCGATGATTATGTTTATCATCA
6615 sha111,
5661 AsnTrpLysGluGluIleLysGlyGluIleLysAsnCysSerPheAsnIleThrThrSer
AATTGGAAAGAAGAAATAAAAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAAGC
TTAACCTTTCTTCTTTATTTTCTCTTTATTTTGGACGAGAAAGTTATAGTGGTGTTCG
6670 mbo11,
5721 IleArgAspLysIleGlnLysGluAsnAlaLeuPheArgAsnLeuAspValValProIle
ATAAGAGATAAGATTGAGAAAGAAATGCACCTTTTCTGTAACCTTGATGTAGTACCAATA
TATTCTCTATTCTAAGTCTTTCTTTTACGTGAAAAAGCATTGGAACACATCATGTTAT
5781 AspAsnAlaSerThrThrThrAsnTyrThrAsnTyrArgLeuIleHisCysAsnArgSer
GATAATGCTAGTACTACTACCACTATACCACTATAGGTTGATACATTGTAACAGATCA
CTATTACGATCATGATGATGGTTGATATGGTTGATATCCAACATGTAAACATTGTCTAGT
6790 sca1,
5841 ValIleThrGlnAlaCysProLysValSerPheGluProIleProIleHisTyrCysThr
GTCATTACACAGGCCTGTCCAAAGGTATCATTGAGCCAATTCATACATTATTGTACC
CAGTAATGTGTCCGGACAGGTTTCCATAGTAAACTCGGTTAAGGGTATGTAATAACATGG
6851 stu1,
5901 ProAlaGlyPheAlaIleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCys
CCGGCTGGTTTTGCGATTCTAAAGTGTAAATAATAAACGTTCAATGGAAAAGGACCATGT
GGCCGACCAAAACGCTAAGATTTACATTATTATTTTCAAGTTACCTTTTCTGTTTAC
5961 ThrAsnValSerThrValGlnCysThrHisGlyIleArgProIleValSerThrGlnLeu
ACAAATGTCAAGCAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTG
TGTTTACAGTCTGTCTACATTACCTTAATCCGGTTATCACAGTTGAGTTGAC
7021 LeuLeuAsnGlySerLeuAlaGluGluGluValValIleArgSerAspAsnPheThrAsn
CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAAC
GACAATTTACCGTCAGATCTCTCTCTCCATCATTAACTAGACTGTTAAAGTGCTTG
7042 mbo11, 7045 mbo11, 7060 bgl11,
7081 AsnAlaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgPro
AATGCTAAAACCATAAATAGTACAGCTGAATGAATCTGTAGCAATTAAGTGTACAAGACCC
TTACGATTTTGGTATTATCATGCTGACTTACTTAGACATCGTTAATTGACATGTTCTGGG
7102 pvu11,
7141 AsnAsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAlaPheHisThrThrGly
AACAAACAATACAAGAAAAGTATCTATATAGGACCAGGGAGAGCATTTCATACAACAGGA
TTGTTGTTATGTTCTTTTTCATAGATATATCCTGGTCCCTCTCGTAAAGTATGTTGCTCT
7199 mbo11,
7201 ArgIleIleGlyAspIleArgLysAlaHisCysAsnIleSerArgAlaGlnTrpAsnAsn
AGAATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGAGCACAATGGAATAAC
TCTTATTATCCTCTATATTCTTTTCTGTAAACATTGTAATCATCTCGTGTACCTATTG
7261 ThrLeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsnAsnLysThrIleVal
ACTTTAGAACAGATAGTTAAAAATTAAGAGAACAGTTTGGGAATAATAAACAAATAGTC
TGAAATCTTGCTATCAATTTTTTAATCTCTTGTCAAACCTTATTATTTTGTATCAG
7321 PheAsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGly
TTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTAGGGG
AAATTAGTTAGGAATCCTCCCTGGGTCTTTAACATTACGTGTCAAATTAACATCTCC
7331 mst11,
7381 GluPhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThr
GAATTTTTCTACTGTAATACAACACAATGTTTAAATAATACATGGAGGTTAAATCACACT
CTTAAAAAGATGACATTATGTTGTGTTGACAAATTATTATGTACCTCCAATTTAGTGTGA
7441 GluGlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsn
GAAGGAACATAAGGAATGACACAATCATCTCCATGTAGAAATAAAACAAATTATAAAC
CTTCCTTGATTTCTTTTACTGTGTAGTATGAGGGTACATCTTATTTTGTTTAATATTG
7501 MetTrpGlnGluValGlyLysAlaMetTyrAlaProProIleGlyGlyGlnIleSerCys
ATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCATTTGGAGGACAAATTAGTTGT
TACACCGTCTTCATCCTTTTCTGTTACATACGGGGAGGGTAACCTCCTGTTTAAATCAACA
7561 SerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAsp
TCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTACAAATGTAACATATGAC
AGTAGTTTATAATGTCCCGACGATAATTGTTCTCTACCACCATGTTACATTGATTACTG

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7621 ThrGluValPheArgProGlyGlyGlyAspMetArgAspAsnTrpArgSerGluLeuTyr
ACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATAT
TGGCTCCAGAAGTCTGGACCTCCTCCTCTATACTCCCTGTAACTCTTCACTTAATATA
7628 mbo11,
7681 LysTyrLysValIleLysIleGluProLeuGlyIleAlaProThrLysAlaLysArgArg
AAATATAAAGTAATAAAAAATTGAACCATTAGGAATAGCACCCACCAAGGCAAAGAGAAGA
TTTATATTTTCACTATTTTAACTTGGAATCCTTATCGTGGGTGGTTCGGTTTCTCTTCT
7736 mbo11,
7741 ValValGlnArgGluLysArgAlaValGlyIleValGlyAlaMetPheLeuGlyPheLeu
GTGGTGCAGAGAGAAAAAGAGCAGTGGGAATAGTAGGAGCTATGTTCTTGGGTCTTG
CACCACGTCTCTCTTTTTCTCGTCACCCTTATCATCCTCGATACAAGGAACCCAAGAAC
7801 GlyAlaAlaGlySerThrMetGlyAlaValSerLeuThrLeuThrValGlnAlaArgGln
GGAGCAGCAGGAAGCACTATGGGCGCAGTGTCTTACGCTGACGGTACAGGCCAGACAA
CCTCGTCTCTCTTCTGATACCCGCGTCACAGTAACTGCGACTGCCATGTCCGGTCTGTT
7861 LeuLeuSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGln
TTATTGTCTGGTATAGTGCAACAGCAGAACAAATTTGCTGAGGGCTATTGAGGCGCAACAA
AATAACAGACCATATCACGTTGTCTGTTGTTAAACGACTCCCGATAACTCCGCGTTGTT
7921 HisLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
CATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCTGGTGTG
GTAGACAACGTTGAGTGTGAGACCCCGTAGTTCTGTCGAGGTCCGTTCTCAGGCGACAC
7981 GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
GAAAGATACCTAAGGGATCAACAGCTCCTAGGGAATTTGGGGTTGCTCTGGAAGACTCATT
CTTCTATGATTCCCTAGTTGTGAGGATCCCTAAACCCCAACGAGACCTTTTGAGTAA
7989 mstII, 7995 binI, 8007 avr2,
8041 CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
TGACCACTGCTGTGCTTGGAAATGCTAGTTGGAGTAATAAATCTCTGGAAGACATTG
ACGTGGTGACGACACGGAACCTTACGATCAACCTCATTATTTAGAGACCTTCTGTAACC
8089 mbo11,
8101 AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
GATAACATGACCTGGATGCACTGGGAAAGAGAAATGACAATTACACAAACACAATATAC
CTATTGTACTGGACCTACGTCAACCTTTCTCTTTAACTGTTAATGTGTTTGTATATG
8161 ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuGluGluLeu
ACCTTACTTGAAGAATCGCAGAACCAACAAGAAAAGAATGAACAAGAATTATTAGAATTG
TGAATGAACCTTCTAGCGTCTTGGTGTCTTTTCTTACTTGTCTTAATAATCTTAAC
8170 mbo11,
8221 AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpLeuTrpTyrIleLys
GATAAGTGGGCAAGTTTGTGGAAATGGTTTAGCATAACAACTGGCTGTGGTATATAAAG
CTATTCACCGTTCAAACACCTTAACCAATCGTATTGTTTGACCGACACCATATATTTCT
8281 IlePheIleMetIleValGlyGlyLeuValGlyLeuArgIleValPheAlaValLeuSer
ATATTGATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTGCTGTGCTTTCT
TATAAGTATTACTATCATCCTCCGAACCATCAAATTCTTATCAAAAACGACACGAAAGA
8341 IleValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrArgLeuProVal
ATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCAATTCAGACCCGCTCCAGTC
TATCACTTATCTCAATCCGTCCCTATGAGTGGAACAGTAAAGTCTGGGCGGAGGGTCAG
8400 avai,
8401 ProArgGlyProAspArgProAspGlyIleGluGluGluGlyGlyGluArgAspArgAsp
CCGAGGGGACCCGACAGGCCCCGACGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGAGAC
GGCTCCCTG666CTGTCCG666CTGCTTAGCTTCTTCTTCCACCTCTCTCTCTCTCTG
8431 mbo11, 8434 mbo11,
8461 ArgSerValArgLeuValAspGlyPheLeuAlaLeuIleTrpGluAspLeuArgSerLeu
AGATCCGTTTGAATTAGTGGATGGATTCTTAGCACTTATCTGGGAAGATCTGCGGAGCCTG
TCTAGGCAAGCTAATCACCTACCTAAGAATCGTGAATAGACCTTCTAGACGCTCGGAC
8503 mbo11, 8505 bg11,
8521 CysLeuPheSerTyrArgArgLeuArgAspLeuLeuLeuIleAlaAlaArgThrValGlu
TCCCTCTTCAGCTACCGCCGTTGAGAGACTTACTCTTGATTGCAGCGAGGACTGTGGAA
ACGGAGAAGTCTGATGGC666GAACTCTGGAATGAGAACTAACGTCTGCTCTGACACCTT
8525 mbo11,

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8581 IleLeuGlyHisArgGlyTrpG...AlaLeuLysTyrTrpTrpSerLeuLeuGlnTyrTrp
 ATTCTGGGGGCACAGGGGGTGGGAAGCCCTCAAATATTGGTGGAGTCTCCTGCAGTATTGG
 TAAGACCCCGTGTCCCCACCCCTTCGGGAGTTTATAACCACTCAGAGGACGTCATAACC
 8629 pst1,
 8641 IleGlnGluLeuLysAsnSerAlaValSerTrpLeuAsnAlaThrAlaIleAlaValThr
 ATTCAAGAACTAAAGAATAGTGTCTGTTAGCTGGCTCAACGCCACAGCTATAGCAGTAACT
 TAAGTCCTTGATTCTTATCAGGACAATCGACCGAGTTGCGGTGTCGATATCGTCATTGA
 8701 GluGlyThrAspArgValIleGluValAlaGlnArgAlaTyrArgAlaIleLeuHisIle
 GAGGGGACAGATAGGGTTATAGAAGTAGCAAAAGAGCTTATAGAGCTATTCTCCACATA
 CTCCCCTGTCTATCCCAATATCTTCATCGTGTCTTCTCGAATATCTCGATAAGAGGTGTAT
 8761 HisArgArgIleArgGlnGlyLeuGluArgLeuLeuLeuOC MetGlyGlyLysTrpSer
 CATAGAAGAATTAGACAGGGCTTGGAAAGGCTTTTGCTATAAGATGGGTGGCAAGTGGTCA
 GTATCTTCTTAATCTGTCCCGAACCTTTCGAAAACGATATTCTACCCACCGTTCACCACT
 8765 mbo11,
 8822 LysArgSerMetGlyGlyTrpSerAlaIleArgGluArgMetArgArgAlaGluProArg
 AAACGTAGTATGGGTGGATGGTCTGCTATAGGGGAAAGAAATGAGACGAGCTGAGCCACGA
 TTTGCATCATACCCACCTACCAGACGATATTCCCTTTCTTACTCTGCTCGACTCGGTGCT
 8882 AlaGluProAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAla
 GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTCGAGACCTGGAAAAACATGGAGCA
 CGACTCGGTGCTCGTCTACCCACCCCTCGTCATAGAGCTCTGGACCTTTTGTACCTCGT
 8883 tthIII1, 8916 ava1 xho1,
 8942 IleThrSerSerAsnThrAlaAlaThrAsnAlaAspCysAlaTrpLeuGluAlaGlnGlu
 ATCACAAGTAGCAATACAGCAGCTACTAATGCTGATTGTGCTGGCTAGAGCACAAGAG
 TAGTGTTCATCGTTATGTCTGTCGATGATTACGACTAACACGGACCGATCTTCGTGTTCTC
 9002 GluGluGluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLys
 GAGGAAGAGGTGGGTTTTCCAGTCAGCTCAGGTACCTTTAAGACCAATGACTTACAAG
 CTCCTTCTCCACCCAAAAGGTGAGTCTGGAGTCTCATGGAAATTCTGGTTACTGAATGTTG
 9005 mbo11, 9029 mstII, 9034 kpnI,
 9062 AlaAlaLeuAspIleSerHisPheLeuLysGluLysGlyGlyLeuGluGlyLeuIleTrp
 GCAGCTTTAGATATTAGCCACTTTTTAAAGAAAAGGGGGGACTGGAAGGGCTAATTTGG
 CGTCGAAATCTATAATCGGTGAAAAATTTTCTTTTCCCCCTGACCTTCCCGATTAAACC
 9085 aha111,
 9122 SerGlnArgArgGlnGluIleLeuAspLeuTrpIleTyrHisThrGlnGlyTyrPhePro
 TCCCAAAGAGAGCAAGAGATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTCCCT
 AGGGTTTTCTTCTGTTCTCTAGGAAGTAGACACCTAGATGGTGTGTGTTCCGATGAAGGGA
 9129 mbo11, 9153 binI,
 9182 AspTrpGlnAsnTyrThrProGlyProGlyIleArgTyrProLeuThrPheGlyTrpCys
 GATTGGCAGAATTACACACAGGCGCAGGGATCAGATATCCACTGACCTTTGGATGGTGC
 CTAACCGTCTTAATGTGTGGTCCCGTCCCTAGTCTATAAGTGAAGTGGAAACCTACCACG
 9210 binI, 9216 ecor5,
 9242 PheLysLeuValProValGluProGluLysValGluGluAlaAsnGluGlyGluAsnAsn
 TTCAAGCTAGTACCAAGTTGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGAACAAC
 AAGTTGATCATGTTCAACTCGGTCTCTTCCATCTTCTCCGGTACTTCTCTCTCTGTTG
 9275 mbo11,
 9302 SerLeuLeuHisProMetSerLeuHisGlyMetGluAspAlaGluLysGluValLeuVal
 AGCTTGTACACCCTATGAGGCTGCATGGGATGGAGGACGCGGAGAAAGAAGTGTAGTG
 TCGAACAATGTGGGATACTCGGACGTACCTACCTCCTGCGCCTCTTCTTCAACATCAC
 9362 TrpArgPheAspSerLysLeuAlaPheHisHisMetAlaArgGluLeuHisProGluTyr
 TGGAGGTTTTGACAGCAAACTAGCATTTTCATCACATGGCCCCGAGAGCTGCATCCGGAGTAC
 ACCTCCAAACTGTGTTTTGATCGTAAAGTAGTGTACCGGGCTCTCGACGTAAGGCTCATG
 9399 ava1, 9417 sca1,
 9422 TyrLysAspCysOP
 TACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGG
 ATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCC
 9482 AGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGCTGCATATAAGCAAGCTG
 TCCGCACCGGACCCGCCCTGACCCCTCACCGCAGGGAGTCTACGACGTATATTCTGTCGAC
 9536 pvu11,

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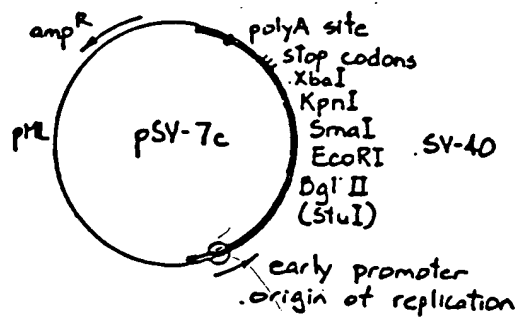
Figure 4
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9542 CTTTTTGCCTGTACTGGGTCTC...GGTTAGACCAGATCTGAGCCTGGGAGC...TCTGGC
GAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCG
9576 bgl111, 9590 sac1,
9602 TAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAATGCTTCAAGTAGTG
ATTGATCCCTTGGGTGACGAATTCGGAGTTATTTGAAACGGAACCTCACGAAGTTCATCAC
9620 af1111, 9634 hind111,
9662 TGTGCCCCTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTATGTCAGTG
ACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCAC
9722 TGGAAAAATCTCTAGCAG
ACCTTTTATAGAGATCGTC

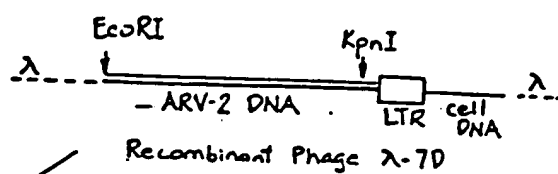
[illegible]

FIGURE 5
2 of 4

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digestion with
KpnI and EcoRI



digestion with
EcoRI and KpnI

ligation

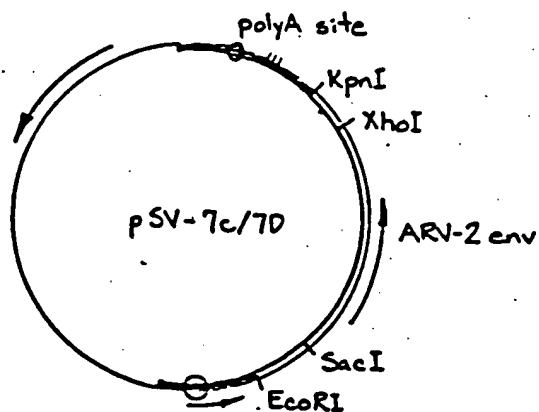
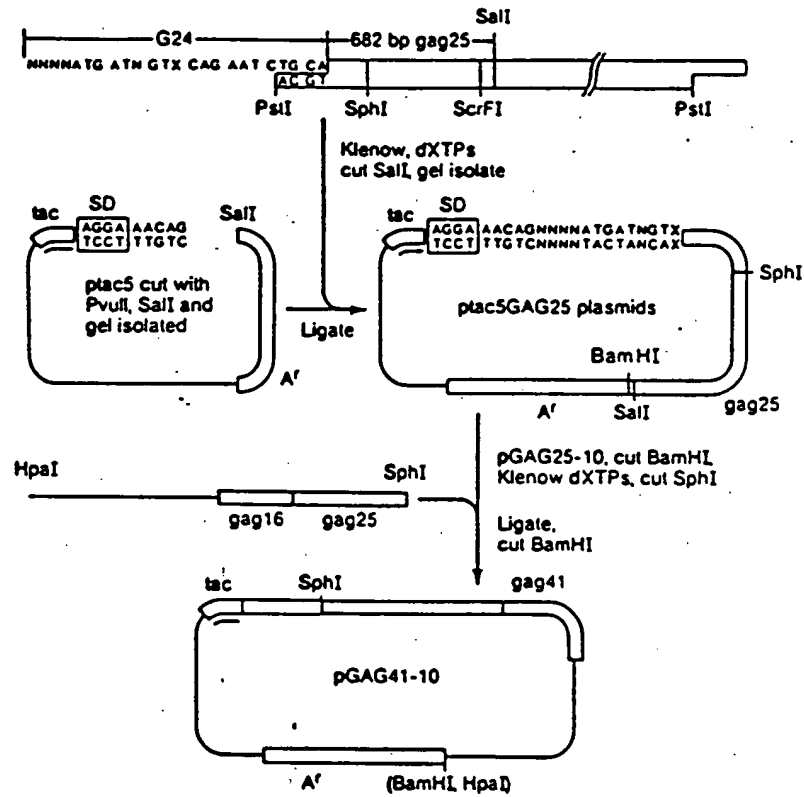


FIG. 6.

Figure 7

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8
FIG.

[illegible]

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FIG. 9

[illegible]

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Figure 10

ARV GAG p16 - synthetic Parts A and B

5' ^{arv 234} MetGlnArgGlyAsnPheArg^{5'}AsnGlnArgLysThrValLysCysPheAsnCysGlyLys
 TATTATGCAAAGAGGTAACCTTCAGGAATCAAAGAAAGACCGTTAAGTGTTCACACTGTGGTAAG
 ATAAATACGTTTCTCCATTGAAGTCCTTAGTTTCTTTCTGGCAATTACAAAAGTTGACACCATTC
 3' ^{arv 235}
 10 mnl1, 23 hinf1, 5'
 63 GluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysAlaCysTrpArgCysGly
 GAAGGTCACATCGCTAAGAACTGTAGAGCTCCAAGAAAGAAGGCTTGTGGAGATGTGGT
 CTTCCAGTGTAGCGATTCTTGACATCTCGAGGTTCTTTCTTCCGAACAACCTCTACACCA
 76 dde1, 88 ban2 hgiA hgiJ11 sac1 sduI, 89 alu1,
 123 ArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIle
 AGAGAAGGTCACCAAATGAAGGACTGTACCGAAAGACAAGCTAACTTCTTGGGTAAGATC
 TCTCTTCCAGTGTTTACTTCTGACATGGCTTTCTGTTCGATTGAAGAACCCATTCTAG
 129 bstE2, 131 hph, 148 rsa1, 161 alu1, 178 bgl11 xho2, 179
 sau3a,
 183 TrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAla
 TGGCCATCTTACAAGGGTAGACCAGGTAACCTTCTTGCAATCCAGACCAGAACCAACCGCT
 ACCGGTAGAATGTTCCCATCTGGTCCATTGAAGAACGTTAAGTCTGGTCTTGGTTGGCGA
 183 bal1 cfr1 hae1, 184 hae111, 199 acc1, 204 apy1 ecor11 sc
 rF1,
 243 ProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLysGlnGlu
 CCACCTGAAGAAAGTTTCAGGTTCCGGTGAAGAAAAGACCACCCCATCTCAAAAGCAAGAA
 GGTGGACTTCTTTCAAAGTCCAAGCCACTTCTTTTCTGGTGGGGTAGAGTTTTCTGTTCTT
 249 mbo11, 267 hph, 270 mbo11,
 303 ProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsnAspPro
 CCAATCGACAAGGAATTGTACCCATTGACCTCTTTGAGATCCTTGTTCGGTAACGATCCC
 GGTTAGCTGTTCTTAAATGAGGTAACCTGGAGAAACTCTAGGAACAAGCCATTGCTAGGG
 307 taq1, 320 rsa1, 331 mnl1, 339 xho2, 340 sau3a, 357 sau3a
 , 361 mnl1, 362 avai xho1,
 363 SerSerGlnOP AM
 TCGAGCCAATGATAG
 AGCTCGGTTACTATCAGCT
 363 taq1, 377 acc1 hind11 sal1

W Z Y

FIG. 11

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E N V

MetSerArgIleAspCysSerAlaThrGluValLeuTrpValThrValTyrTrpGlyValProVal 51
ATGTCAGAAATCATGTAGTGTACAGAAATTTGGGTACACATTTATTATGAGTACCTGTG

TrpLeuGluValThrThrLeuPheCysAlaSerAspAlaArgAlaIleAspThrGluValValMetIleValThrAlaThrHisAlaCysValProThrAspProAsnProGlnGluVal 91
TGGAAAGAACCACTACCACTCTATTTTGTGTCATCAGATGCTAGACATATGATACAGAGGTACATAATGTTTGGGCACACATGCTGTGTACCCACAGCCCAACCCACAGAGATA

ValLeuGluValAsnValThrGluAsnPheAsnMetTrpLysAsnAsnMetValGluMetGlnGluValIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThrPro 131
GTATTGGGAAATGTGACAGAAATTTAACATGTGAAAAATTAACATGCTAGACAGATGCGAGGATATAATCAGTTTATGGGATCAAGGCTAAAGGCTGTGTAAATTTAACCCCA

LeuCysValThrLeuAsnCysThrAspLeuGluLysAlaThrAsnThrAsnSerSerAsnTrpLysGluValIleLysGluValIleLysAsnCysSerPheAsnIleThrThrSerIle 171
CTCTGTGTACTTTAAATTGCACGTATTTGGGAAGGCTACTAATACCAATAGTAGTAATTCGAAGAGAAATAAAGGAGAAATAAAGAACTGCTCTTCAATATATCACCACAGCAT

ArgAspLysIleGlnLysGluValAsnAlaLeuPheArgAsnLeuAspValProIleAspAsnAlaSerThrThrThrAsnTrpThrAsnTrpArgLeuIleMetCysAsnAspSerVal 211
AGAGATAAGATTCAGAAAGAAATGCACTTTTCTGTAACCTTGATGCTAGTACCAATAGATAATGCTAGTACTACTACCAATATACCACTATAGGTTGATACATTTGTAAACAGATCAGTC

IleThrGlnAlaCysProLysValSerPheGluProIleProIleMetIleIleIleIleIleLysCysAsnAsnLysThrPheAsnGluLysGluProCysThr 251
ATTACACAGGCTTCCCAAGGATCATTTGAGCCATTTCCCATACATATTGTTACCCGCGCTGTTTCCGATTTCTAAGGTGTAATAAAGCTTCAATGGAAAGGAGCCATGTACA

AsnValSerThrValGlnCysThrMetIleValIleArgProIleValSerThrGlnLeuLeuAsnGluSerLeuAlaGluValIleValIleArgSerAspAsnPheThrAsnAsn 291
AATGTCAGCAGTACATGTACATGGAATTAGCCCAATAGTGTCACTCACTGCTTAAATGCGAGCTAGCAGAAAGAGGCTAGTAATTAGATCTGACAAATTTCCAGGACAAAT

AlaLysThrIleIleValGlnLeuAsnMetSerValAlaIleAsnCysThrArgProAsnAsnThrArgLysSerIleIleIleGluProGluArgAlaPheMetIleThrThrGlyArg 331
GCTAAACCATTAATAGTACAGCTGAATGAACTGTAGCAATTAACGTACAGAGCCCAACACATACAGAAAGAGTATCTATAGGACAGGAGAGCATTTTCATACAGAGAGAGA

IleIleGluAspIleArgLysAlaMetCysAsnIleSerArgAlaGlnTrpAsnAsnThrLeuGluGlnIleValLysLysLeuArgGluGlnPheGluAsnAsnLysThrIleValIlePhe 371
ATAATAGGAGATTAAGAAAGCAGATTTGTACATTTAGTACAGCAGATGGAATTAACACTTTAGAACAGATAGTTAAGAAATTAAGACAGAGTTTGGGATAATAAAGCAATAGTCTTT

AsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGlyGluPhePheTrpCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnMetIleThrGlu 411
AATCAATCTTCAGAGAGGAGCCAGAAATTTGATATGACAGCTTTAATTTAGAGGAGAAATTTTCTACTGTAATACAGCAACTGTTTAAATATACATGAGGCTTAATATCAGACTGAA

GlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsnMetTrpGlnGluValGluLysAlaPheTrpAlaProProIleGluLysGluIleSerCysSer 451
GGAATAAGGAATGACACAATCATCTCCCATGTAGATAAAGCAATATATACATGTGCGAGAGAGTAGAAGCAATGTATGCCCTCCCATTTGAGAGAGCAAAATTAGTGTGTTCA

SerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAspThrGluValPheArgProGluLysGlyLysMetArgAspAsnTrpArgSerGluLeuThrLys 491
TCAATATTACAGGCTGCTATTAAACAGAGATGGTGTACAAATGTAACATTAATGACACCGAGGCTTTCAGACCTGGAGGAGAGATATGAGGAGCAATTTGAGAGAGTGAATTATATATAA

TyrLysValIleLysIleGluProAsnSerValSer 531
TATAAGTAATAAATTAATTAACCAATTCGATATCTTGA

PKY Promoter

PKY Terminator

FIG. 11

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Nucleotide
positions
relative to
FIGURE 5.

MetIleAspLysAlaGlnGluGluHisGluLysTyrHisSerAsnTrp
 1 AGGXAAACAG:::ATGAT:GA:AAGGCACAA6AAGAACATGAGAAATATCACAGTAATTGG
 TCCXTTGTCT:::TACTA:CT:TTCCGTGTTCTTCTTGTACTCTTTATAGTGTCATTAACC

32 mbo11, 38 nla111,
 3820 62 ArgAlaMetAlaSerAspPheAsnLeuProProValValAlaLysGluIleValAlaSer
 AGAGCCATGGCTAGTGATTTTAACTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGC
 TCTCGGTACCGATCACTAAAATTGGACGGTGGACATCATCGTTTTCTTTATCATCGGTCTG

66 nco1, 67 nla111, 118 nspBII pvu11, 119 alu1,
 3880 122 CysAspLysCysGlnLeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGly
 TGTGATAAATGTGAGCTAAAAGGAGAGCCATGCATGGACAAGTAGACTGTAGTCCAGGA
 ACACATTTTACAGTCTGATTTTCTCTTCTGCTACGTACCTGTTCTGACATCAGGTCTCT

135 alu1, 151 nla111, 152 nsi1 ava3, 155 nla111, 164 acc1, 1
 76 apy1 bstXI ecor11 scrF1,
 3940 182 IleTrpGlnLeuAspCysThrHisLeuGluGlyLysIleIleLeuValAlaValHisVal
 ATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCCTGGTAGCAGTTTCATGTA
 TATACGTTGATCTAACATGTGTAGATCTTCTTTTAAATAGGACCATCGTCAAGTACAT

198 rsa1, 205 xba1, 223 apy1 ecor11 scrF1, 236 nla111,
 4000 242 AlaSerGlyTyrIleGluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyr
 GCCAGTGGATATATAGAAGCAGAGATTATCCAGCAGAGACAGGGCAGGAAACAGCATAT
 CGGTACCTATATATCTTCTCTTCAATAAGGTCTCTCTGTCCCGTCTTTGTCTGTATA

263 xmn1,
 4060 302 PheLeuLeuLysLeuAlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySer
 TTTCTCTTAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGC
 AAAGAGAATTTTAAATCGTCTTCTACCGGTCAATTTTGTATGTATGTCTGTTACCGTCTG

321 mbo11, 326 bal1 cfr1 hae1, 327 hae111, 357 bbv fnu4h1,
 4120 362 AsnPheThrSerThrThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPhe
 AATTTCAACAGTACTACGGTTAAGGCCGCTGTTGTTGGGCAGGGATCAAGCAGGAATTT
 TTAAAGTGGTCTATGATGCCAATTCCGGCGGACAACCCGTCCTAGTTCGTCTCTTAA

366 hph, 371 sca1, 372 rsa1, 385 hae111, 386 fnu4h1 nsb11, 4
 05 bin1, 406 dpn1 sau3a,
 4180 422 GlyIleProTyrAsnProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLys
 GGCATTCCTACAAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAATGAATTAAAG
 CCGTAAGGGATGTTAGGGGTTTCAGTTCTCATCATCTTAGATACTTATTACTTAATTTCT

423 bsm1, 458 hinf1,
 4240 482 LysIleIleGlyGlnValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAla
 AAAATTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCA
 TTTTAATATCTGTCCATTCTCTAGTCCGACTTGTGGAATTCTGTCGTATGTTTACCGT

503 dpn1 sau3a, 518 afl11, 530 rsa1,
 4300 542 ValPheIleHisAsnPheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArg
 GTATTTCATCCACAATTTTAAAGAAAGGGGGGATTGGGGGATACAGTGCAGGGGAAAGA
 CATAAGTAGGTGTTAAATTTTCTTTTCCCCCTAACCCCTATGTCACGTCCCCTTTCT

547 fok1, 557 sha111,
 4360 602 IleValAspIleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLys
 ATAGTAGACATAATAGCAACAGACATACAACTAAAGAACTACAAAGCAAATTAACAAA
 TATCATCTGTATTATCGTTGTCTGTATGTTTGATTTCTTGATGTTTTCTTTAATGTTTT

605 acc1,
 662 IleGlnAsnPheArgValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAla
 ATTCAAAATTTTTCGGGTTTATTACAGGGACAACAAAGATCCCCTTTGGAAAGGACCAGCA

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4480 722 LysLeuLeuIrpLysGlyGlyGlyAlaValValIleGlnAspAsnSerAspIleLysVal
 AAGCTTCTCTGGAAAGGTGAAGGGGCAGTAGTAATAACAATAATAGTGACATAAAAGTA
 TTCGAAGAGACCTTTCCACTTCCCCGTCATCATTATGTTCTATTATCACTGTATTTTCAT
 722 hind111, 723 alu1, 737 hph,
 4540 782 ValProArgArgLysAlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAsp
 GTGCCAAGAAGAAAAGCAAAAATCATTAGGGGATTATGGAAAACAGATGGCAGGTGATGAT
 CACGGTTCTTCTTTTCGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTA
 789 mbo11, 833 hph,
 4600 842 CysValAlaSerArgGlnAspGluAspAM
 TGTGTGGCAAGTAGACAGGATGAAGATTAGTCGACGGAATTCTTTAGTAAACACC
 ACACACCGTTCATCTGTCCTACTCCTAATCAGCTGCCCTTAAGAAATCATTTTGTGG
 852 acc1, 859 fok1, 863 mnl1, 871 acc1 hind11 sal1, 872 taq1
 , 878 ecor1,

FIGURE 12

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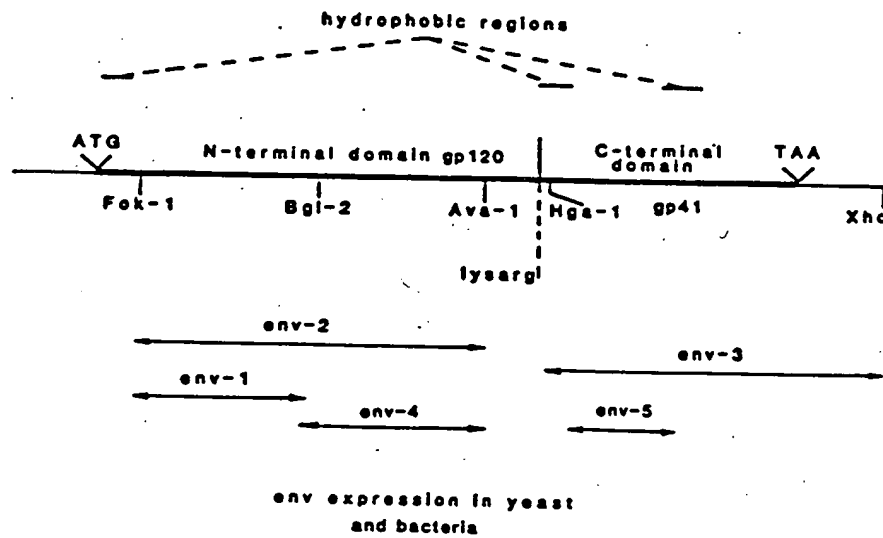


FIGURE 13

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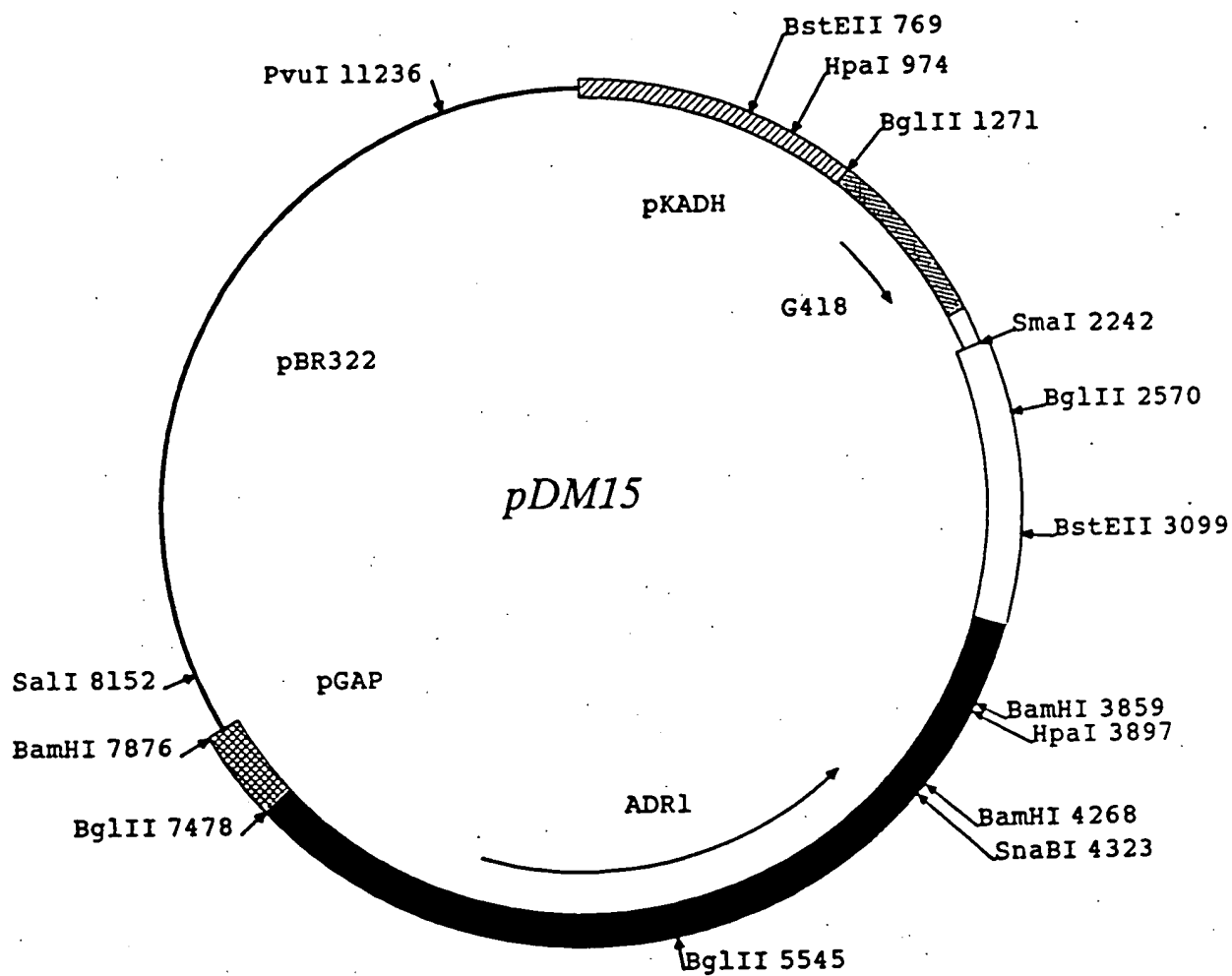


FIGURE 14

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- SCD
 MetAlaThrLysAlaValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsn
 1 CATGGCGACGAAGGCCGTGTGCTGCTGAAGGGCGACGGCCAGTGCAGGGCATCATCAAT
 CGCTGCTTCGGGCACACGCACGACTTCCCGCGCCGGTCACGTCCCGTAGTAGTTA

 PheGluGlnLysGluSerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThr
 62 TTCGAGCAGAAGGAAAGTAATGGACCAGTGAAGGTGTGGGGAAGCATTAAAGGACTGACT
 AAGTCGTCTTCCCTTCATTACCTGGTCACCTCCACACCCCTTCGTAAATTTCCTGACTGA

 GluGlyLeuHisGlyPheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSer
 122 GAAGGCCTGCATGGATTCCATGTTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCACT
 CTTCCGGACGTACCTAAGGTACAAGTACTCAAACCTCTATTATGTCTGCGCAGCATGGTCA

 AlaGlyProHisPheAsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArg
 182 GCAGGTCCCTCACTTTAATCCTCTATCCAGAAAACACGGTGGGGCCAAAGGATGAAGAGAGG
 CGTCCAGGAGTGAATTAGGAGATAGGTCTTTTGTGCCACCCGGTTTCTACTTCTCTCC

 HisValGlyAspLeuGlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIle
 242 CATGTTGGAGACTTGGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT
 GTACAACCTCTGAACCGTTACACTGACGACTGTTTCTACCAACCCGCTACACAGATAA

 GluAspSerValIleSerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValVal
 302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTGCATCATTGGCCGCACACTGGTGGTC
 CTTCTAAGACACTAGAGTGAGAGTCTCTGTGAACGTAGTAACCGGCGTGTGACCACCG

 HisGluLysAlaAspAspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsn
 362 CATGAAAAGCAGATGACTTGGGCAAGGTGGAATGAAGAAAGTACAAAGACAGGAAC
 GTACTTTTTCTCTACTGAACCGTTTCCACCTTACTTCTTTCTATGTTTCTGTCTCTTG

 ENV 53
 AlaGlySerArgLeuAlaCysGlyValIleGlyIleAlaMetAlaIleGluAlaGlnGln
 422 GCTGGAAGTCGTTTGGCTTGTGTGTAATTGGGATCGCCATGGCTATCGAAGCTCAACAA
 CGACCTTCAGCAAAACCGAACACCATTAACCTTAGCGGTACCGATAGCTTCGAGTTGTT
 As1
 HisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
 482 CACTTGCTGCAGTTGACCGTTTGGGTATCAAGCAGTTGCAGGCTAGAGTTTGGCTGTT
 GTGAACGACGTCACTGGCAAACCCCATAGTTCTGTCAACGTCCGATCTCAAAACCGACAA

 GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
 542 GAAAGATACCTTGAGAGATCAACAAATTGTTGGGTATCTGGGTTGTTCTGGTAAGTTGATT
 CTTTCTATGAATCTCTAGTTGTTAAACAACCCATAGACCCCAACAGACCATTCAACTAA

 CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
 602 TGTAACACCGCTGTTCCCTGGAAACGCTTCTTGGTCTAACAAGTCTTTGGAAGACATCTGG
 ACATGGTGGCGACAAGGGACCTTGGGAAGAACCAGATTGTTTCAAGAACCTTCTGTAGACC

 AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
 662 GACAACATGACCTGGATGCAATGGGAAAGAGAAATCGACAACATACCAACACCATCTAC
 CTGTTGTACTGGACCTACGTTACCTTTCTCTTAGCTGTGTGATGTGTTGTTGTTAGATG

 ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
 722 ACCTTGTTGGAGGAATCTCAAAACCAAGAAAAGAACGAACGAAGAAATTGTTGGAAATG
 TGGAACAACCTCCTTAGAGTTTGGTTGTTCTTTCTTCTTGTGTTCTTAACAACCTTAAC

 AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpAM
 782 GACAAGTGGGCAAGCTTGTGGAACTGTTCTCTATCACCAACTGGTAG
 CTGTTACCCGTTTGAACACCTTGACCAAGAGATAGTGGTTGACCATCAGCT

Translated Mol. Weight = 30414.22

FIGURE 15

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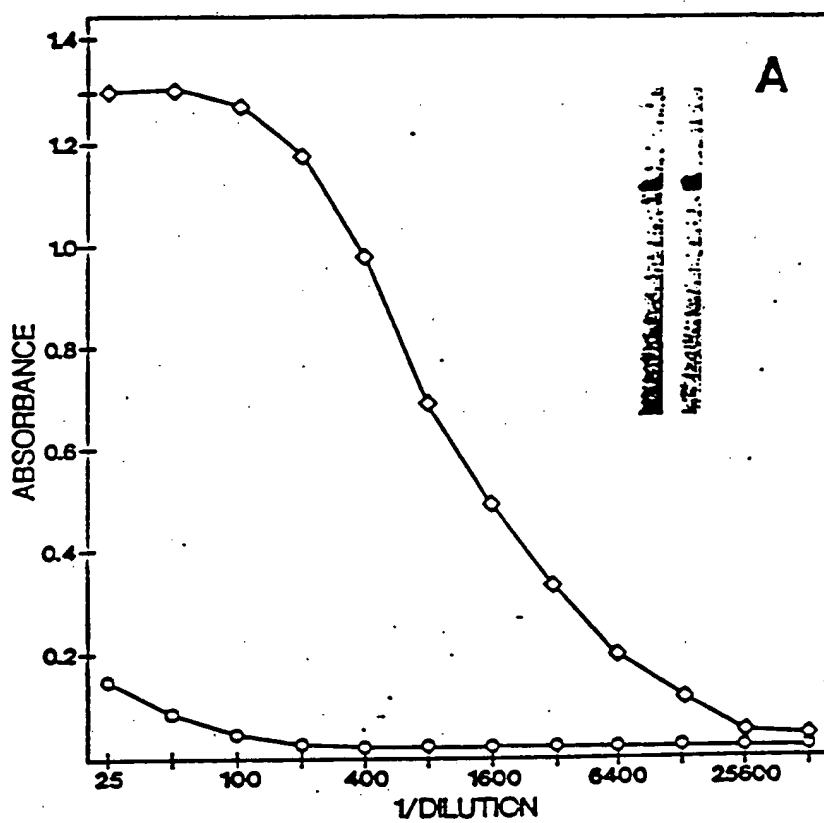


FIGURE 16

1 of 2

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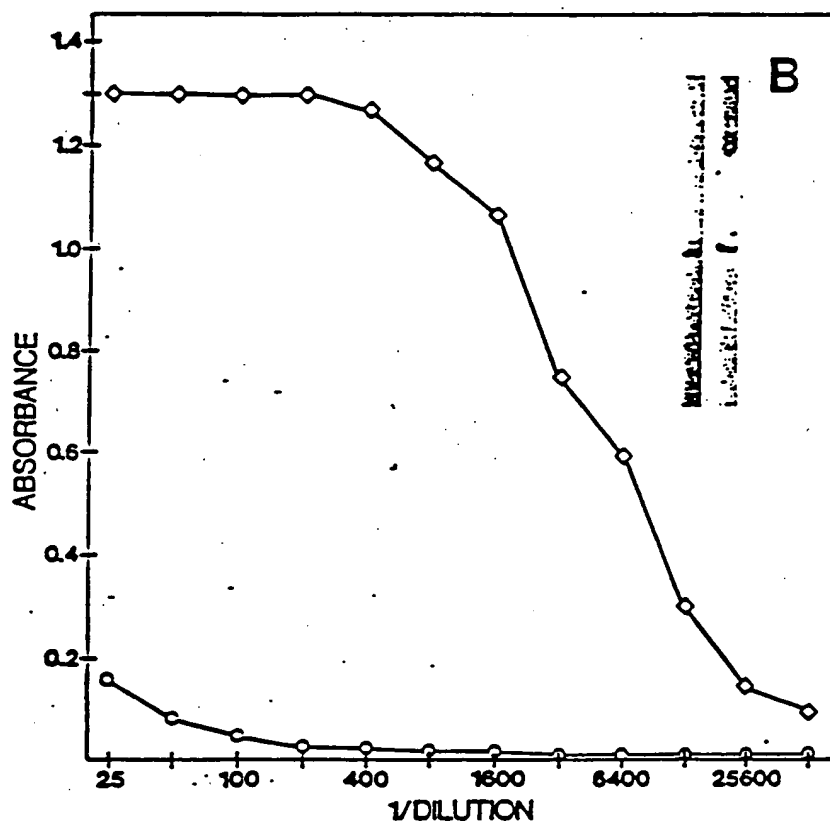


FIGURE 16

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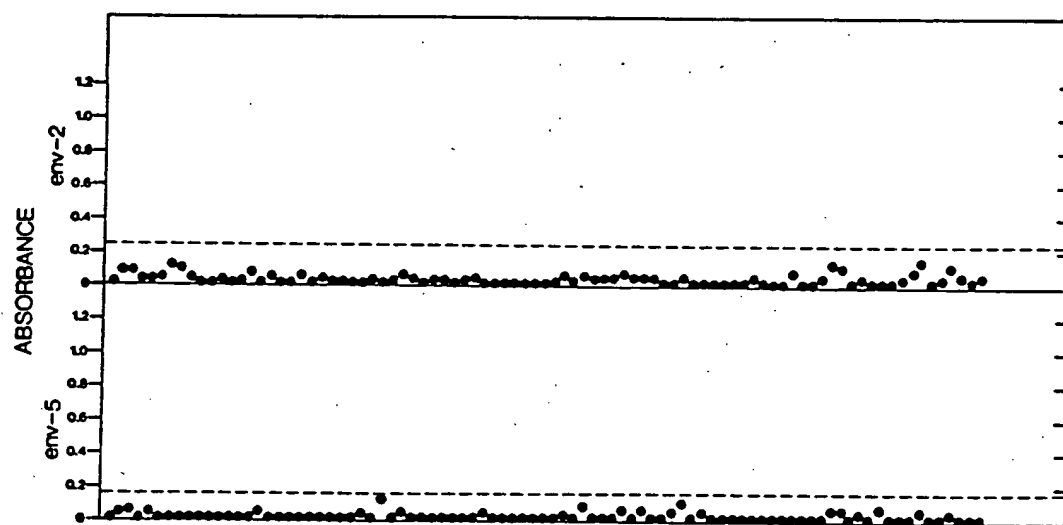


FIGURE 17

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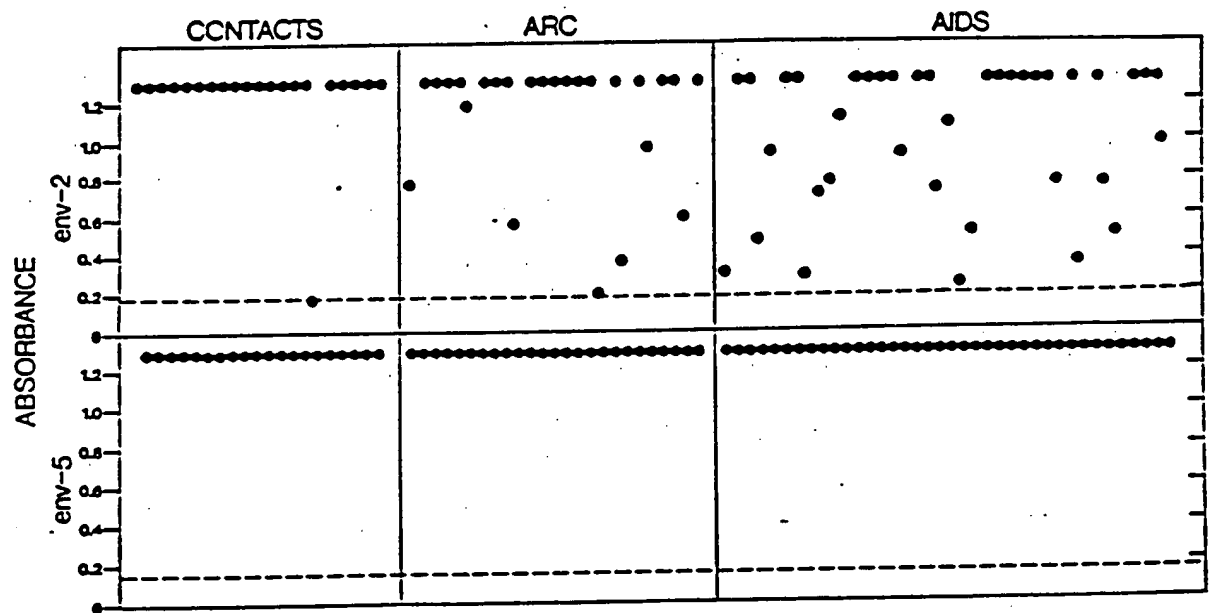


FIGURE 18

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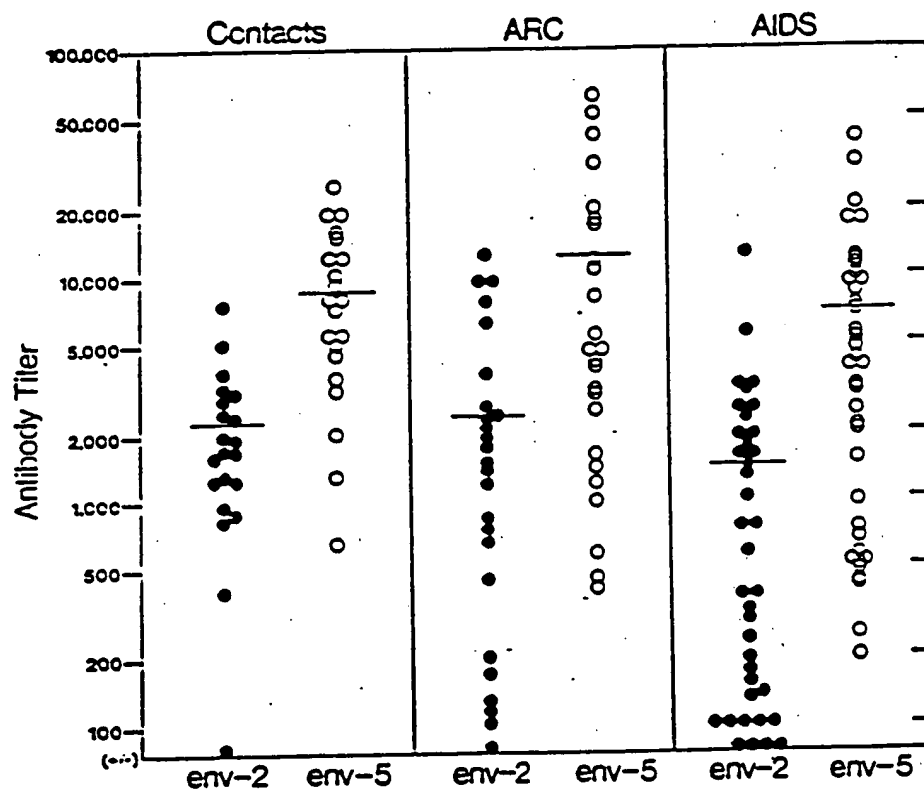


FIGURE 19

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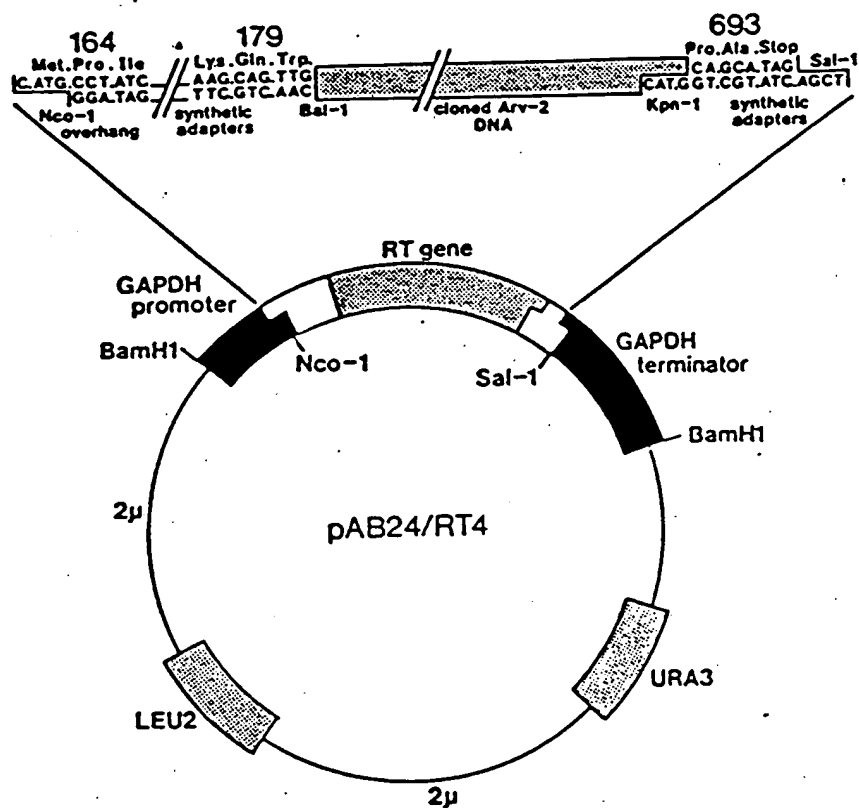


FIGURE 20

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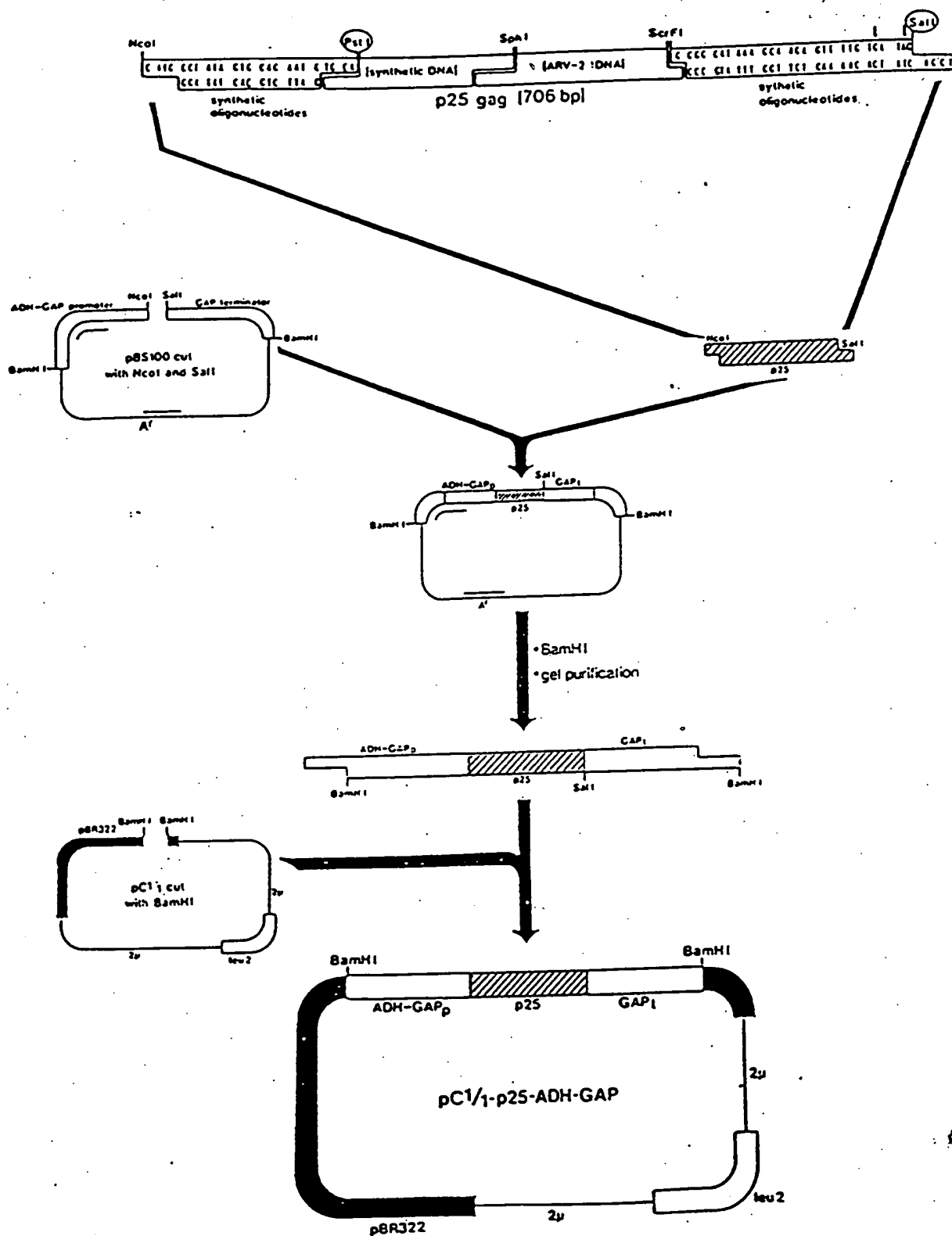


FIGURE 21

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1 10
Met Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln
C ATG CCT ATA GTG CAG AAT CTG CAG GGG CAA ATG GTA CAT CAG

20
Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
GCC ATA TCA CCT AGA ACT TTA AAT GCT TGC GTA AAA GTA GTA GAA

30 40
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
GAA AAG GCT TTC AGC CCA GAA GTA ATA CCC ATG TTT TCA GCA TTA

50
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
TCA GAA GGA GCC ACC CCT CAA GAT TTA AAC ACC ATG CTA AAC ACA

60 70
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile
GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACT ATC

80
Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala
AAT GAG GAG GCT GCC GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA

90 100
Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp
GGG CCT ATT GCA CCA GGC CAA ATG AGA GAA CCA AGG GGA AGT GAC

110
Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
ATA GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG

120 130
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp
ACA AAT AAT CCA CCT ATC CCA GTA GGA GAA ATC TAT AAA AGA TGG

140
Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
ATA ATC CTG GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC

150 160
Ser Ile Leu Asn Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp
AGC ATT CTG GAC ATA AGA CAA GCA CCA AAG GAA CCC TTT AGA GAT

170
Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
TAT GTA GAC CGG TTC TAT AAA ACT CTA AGA GCC GAA CAA GCT TCA

180 190
Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn
CAG GAT GTA AAA AAT TGG ATG ACA GAA ACC TTG TTG GTC CAA AAT

200
Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
GCA AAC CCA GAT TGT AAG ACT ATT TTA AAA GCA TTG GGA CCA GCA

210 220
Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG GGA GTC GGG GGA

230 232
Pro Gly His Lys Ala Arg Val Leu OP
CCC GGG CAT AAA GCA AGA GTT TTG TGA TAG

Translated Mol. Weight = 25700.75

FIGURE 22

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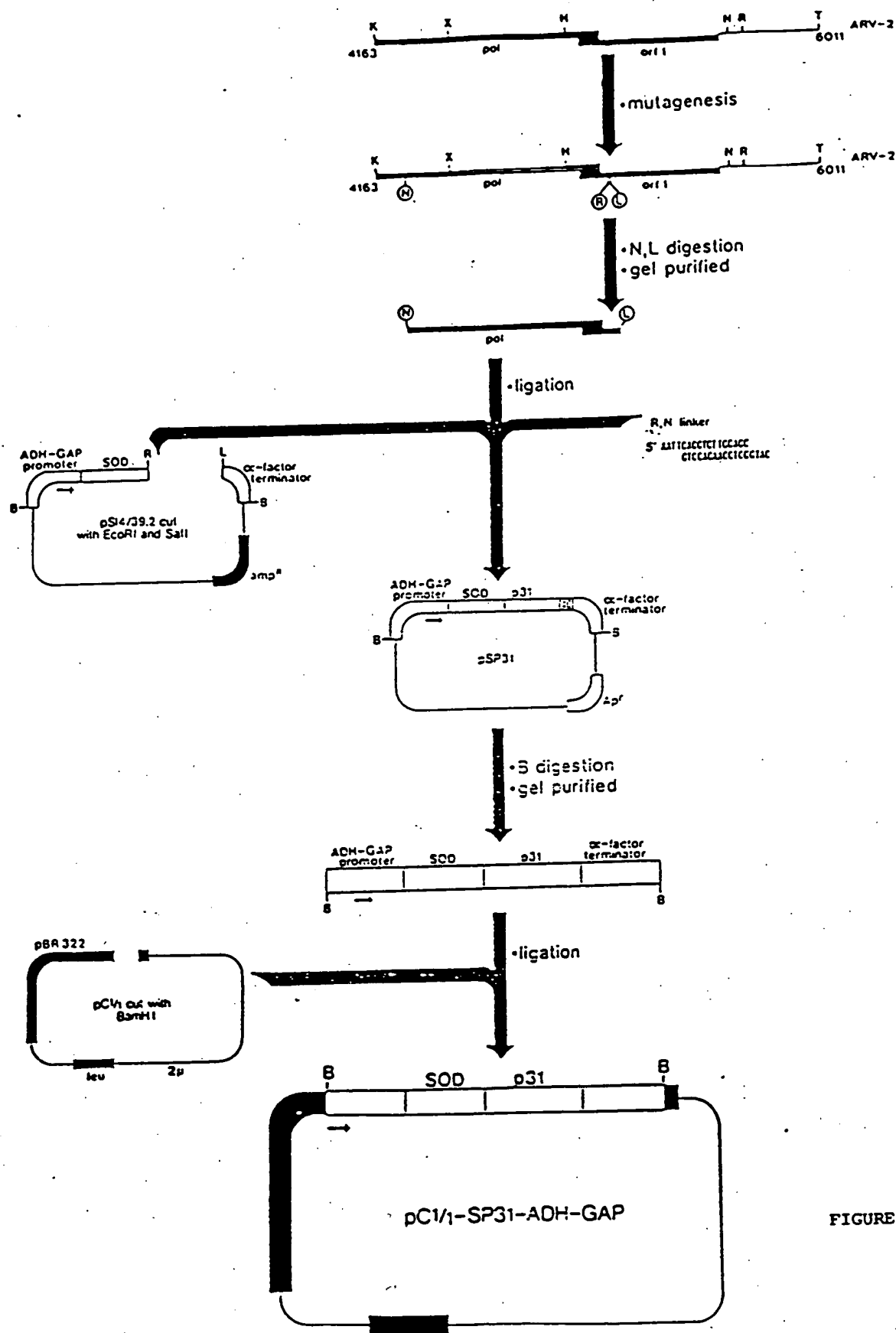


FIGURE 23

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500 -->
 MetAlaThrLysAla
 ATGGCTACAAAGGCT
 TACCGATGTTTCCGA

1383 ValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsnPheGluGlnLysGlu
 GTTTGTGTTTTGAAGGGTGACGGCCAGTTCAGGTATTATTAACTTCGACGAGAAGGAA
 CAAACACAAAACCTTCCCACTGCCGGGTCAAGTTCATAATAATTGAAGCTCGTCTTCTT

1443 SerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThrGluGlyLeuHisGly
 AGTAATGGACCACTGAAGGTGTGGGGAAGCATTAAAGGACTGACTGAAGCCCTGCATGGA
 TCATTACCTGGTCACCTCCACACCCCTTCGTAATTTCTGACTGACTTCGGACGTACCT

1503 PheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSerAlaGlyProHisPhe
 TTCCATGTTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCACTGCAGGTCTCCTTT
 AAGGTCCAGAGTACTCAAACTCTATTATGTGTCGTCGACATGGTCAGCTCAGGAGTGAAA

1563 AsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArgHisValGlyAspLeu
 AATCCTCTATCCAGAAAACACGGTGGGCCAAAGGATGAAGAGAGGCGATGTTGGAGACTTG
 TTAGGAGATAAGTCTTTTGTGCCACCCGGTTTCTACTTCTCTCCGTACAACTCTGAAC

1623 GlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIleGluAspSerValIle
 GGCAATGTGACTGCTGCAAAAGATGGTGTGGCCGATGTGTCTATTGAAGTCTGTGATC
 CCGTTACACTGACGACTGTTTCTACACACCCGCTACACAGATAACTTCTAAGACACTAG

1683 SerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValValHisGluLysAlaAsp
 TCACCTCTCAGGAGACCATTTGCATCATTGGCCGACACTGGTGGTCCATGAAAAGAGCAT
 AGTGAGAGTCTCTGTAACGTAGTAACCGGCGTGTGACCACAGGTACTTTTTCTGTCTA

1743 AspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsnAlaGlySerArgLeu
 GACTTGGGCAAAAGTGGAAATGAAGAAAGTACAAAGACAGGAAACCTGGAAGTCTGTTG
 CTGAACCCGTTTCCACCTTACTTCTTTTCTGTCCTTTGCGACCTTCAGCAAAAC

1803 AlaCysGlyValIleGlyIleAlaGlnAsnSerGlyValGlyAlaMetAlaMetAlaSer
 GCTTTGTGGTGAATTTGGGATCGCCAGAAATTCAGGTGTTGGAGCCATGGCCATGGCTAGT
 CGAACACCACATTAAACCTTAGCGGGTCTTAAGTCCACAACCTCGGTACCGGTACCGATCA

1863 AspPheAsnLeuProProValValAlaLysGluIleValAlaSerCysAspLysCysGln
 GATTTTAACTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTGAG
 CTAAATTTGGACGGTGGACATCATCGTTTTCTTTATCATCGGTGACACTATTACAGTC

1923 LeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAsp
 CTAAAGGAGAGGCGCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCACTAGAT
 GATTTTCTCTCGGTACGTACCTGTTTCTCTGACATCAGGTCTTATACCTTGTATCTA

1983 CysThrHisLeuGluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIle
 TGTACACATCTAGAAGGAAAAATTTCTCTGGTAGCAGTTCTGTAGCCAGTGGATATATA
 ACATGTGTAGATCTTCTTTTTAATAGGACCATCGTCAAGTACATCGGTACCTATATAT

2043 GluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLysLeu
 GAAGCAGAAGTATTTCAGCAGAGACAGGGCAGGAACAGCATATTTCTCTTAAATTA
 CTTCTCTTCAATAAGGTCTGTCTGTCCCGTCTTTGTGCTATAAAGAGAATTTAAT

2103 AlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySerAsnPheThrSerThr
 GCAGGAAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGCAATTTCCACGACTCT
 CGTCTCTTCTACCGGTCTATTTTGTATGTATGTCTGTTACCGTCTTAAAGTGGTCATGA

2163 ThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsn
 ACSGTTAAGGCCCGCTGTTGGTGGCAGGGATCAAGCAGGAATTTGGCATTCCTTACAAT
 TGCCAATTCGGGCGGACAACCAACCCGTCCTAGTTCTGTCCTTAAACCGTAAGGGATGTTA

2223 ProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGln
 CCCCCAAGTCAAGGAGTAGTAGAATCTATGAATAATGAATTAAGAAAAATTATAGGACAG
 GGGGTTTCAGTTCTCTCATCTTAGATACCTTATTACTTAAATTTCTTTAATATCTGTG

2283 ValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsn
 GTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCTCCACAAT
 CATCTCTAGTCCGACTTGTGAATTTCTGTCGTATGTTTACCGTCATAAGTAGGTGTTA

2343 PheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIle
 TTTAAAAGAAAAGGGGGGATTGGGGGATACAGTGCAGGGGAAAGAAATAGTAGACATAATA
 AAAATTTCTTTTCCCCCTAACCCCTATGTACGTCCTCTTCTTATCATCTGTATTAT

2403 AlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArg
 GCAACAGACATACAACTAAAGAACTACAAAAGCAAATACAAAAATTCAAAATTTTCGG
 CSTTGTCTGTATGTTGATTTCTTGTATGTTTCTGTTAATGTTTAAAGTTTTAAAGGCC

2463 ValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLys
 GTTTATTACAGGGCAACAAAGATCCCCCTTTGGAAAGGACCAAGGCTTCTCTGGAAG
 CAAATAATGTCCTCTGTTGTTCTAGGGGAAACCTTCTGCTGTTTGAAGAGACCTTT

2523 GlyGluGlyAlaValValIleGlnAspAsnSerAspIleLysValValProArgArgLys
 GGTGAAGGGGCACTAGTAATACAAAGATAATGACATAAAAGTAGTGCCCAAGAGAAAA
 CCACCTCCCCCTCATCATTATGTTCTATTATCACGTATTTTCTATCACGGTCTTCTTTT

2583 AlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArg
 GCAAAATCATTAGGCAATTATGGAAAAAGATGGCAGGTGATGTTGTGTGGCAAGTAGA
 CGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTAACACACCTTCTATCT

2643 GlnAspGluAspAsn
 CAGGATGAGGATTAG
 GTCTACTCTAATC

FIGURE 24

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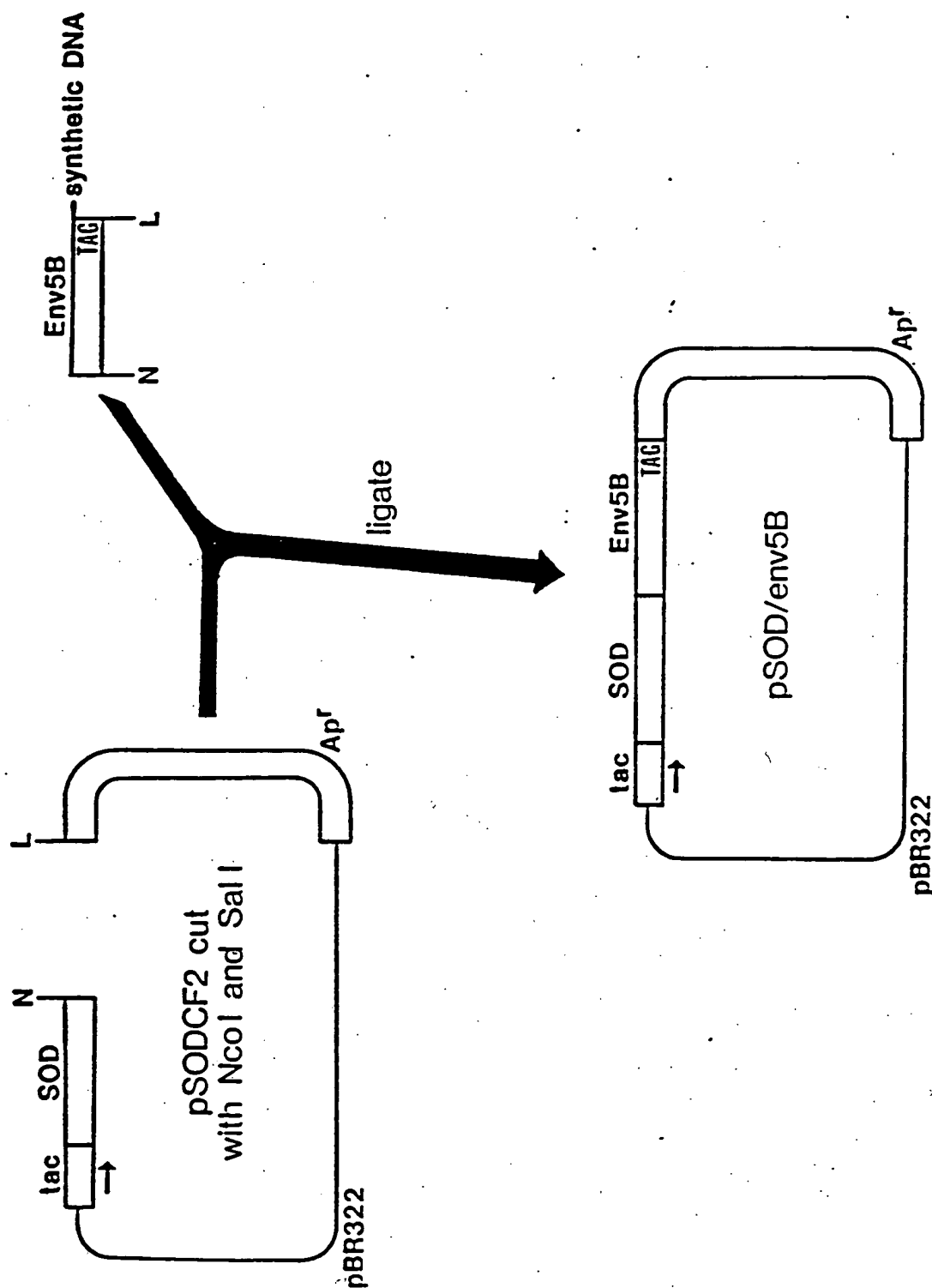


FIGURE 25

Sequence of SOD/env-4

1-000

[illegible]

CONFIDENTIAL

[illegible]

CONFIDENTIAL

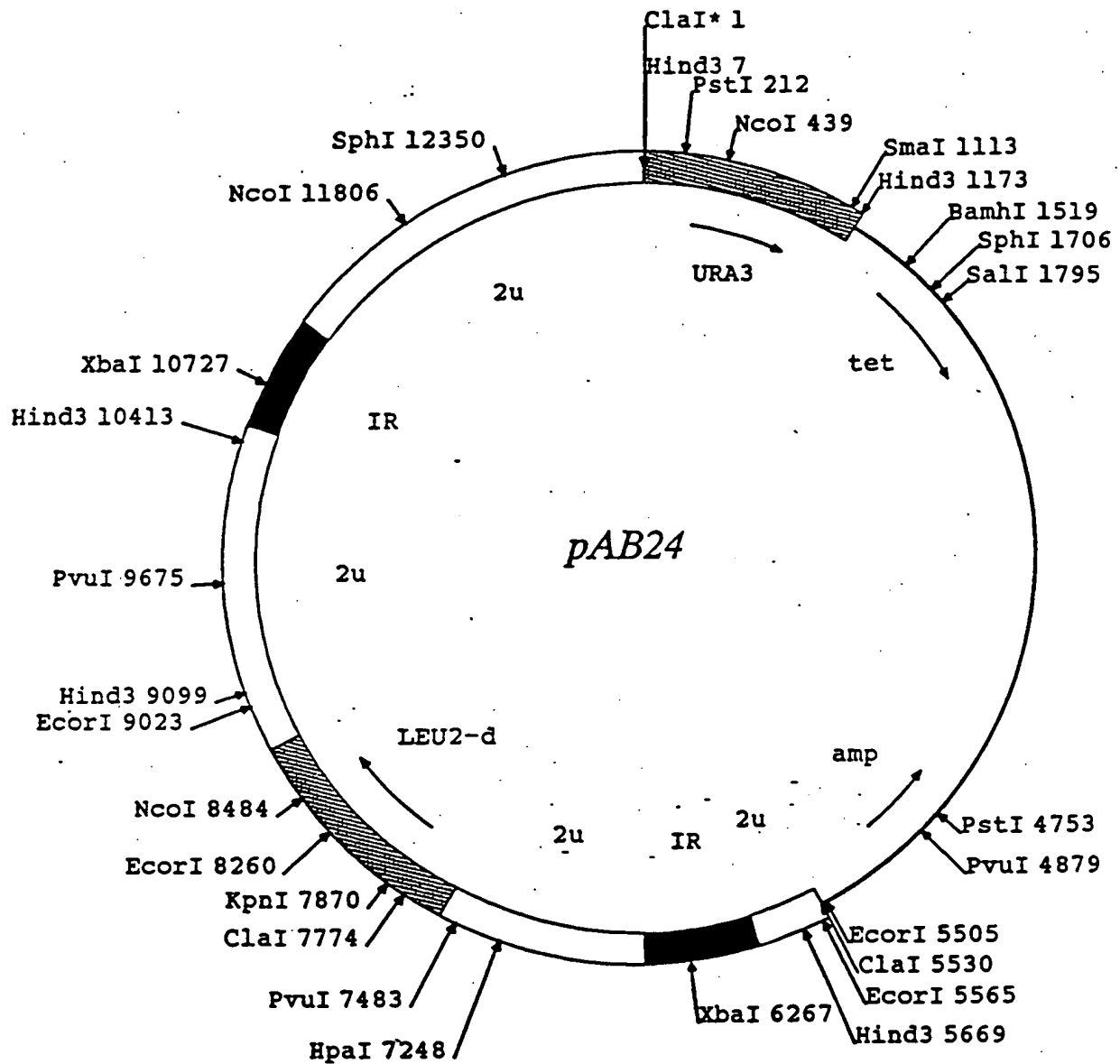


FIGURE 27

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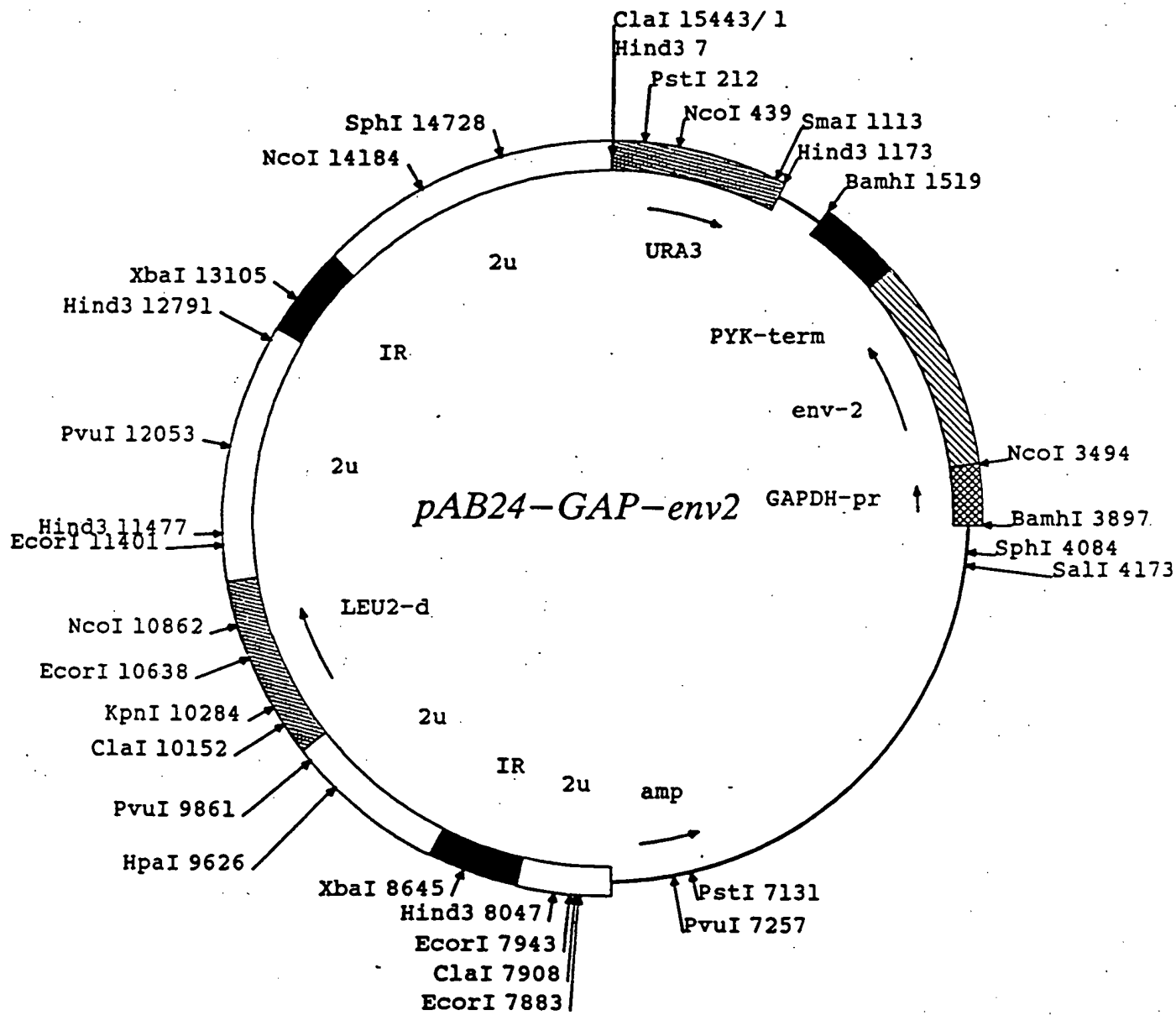


FIGURE 28

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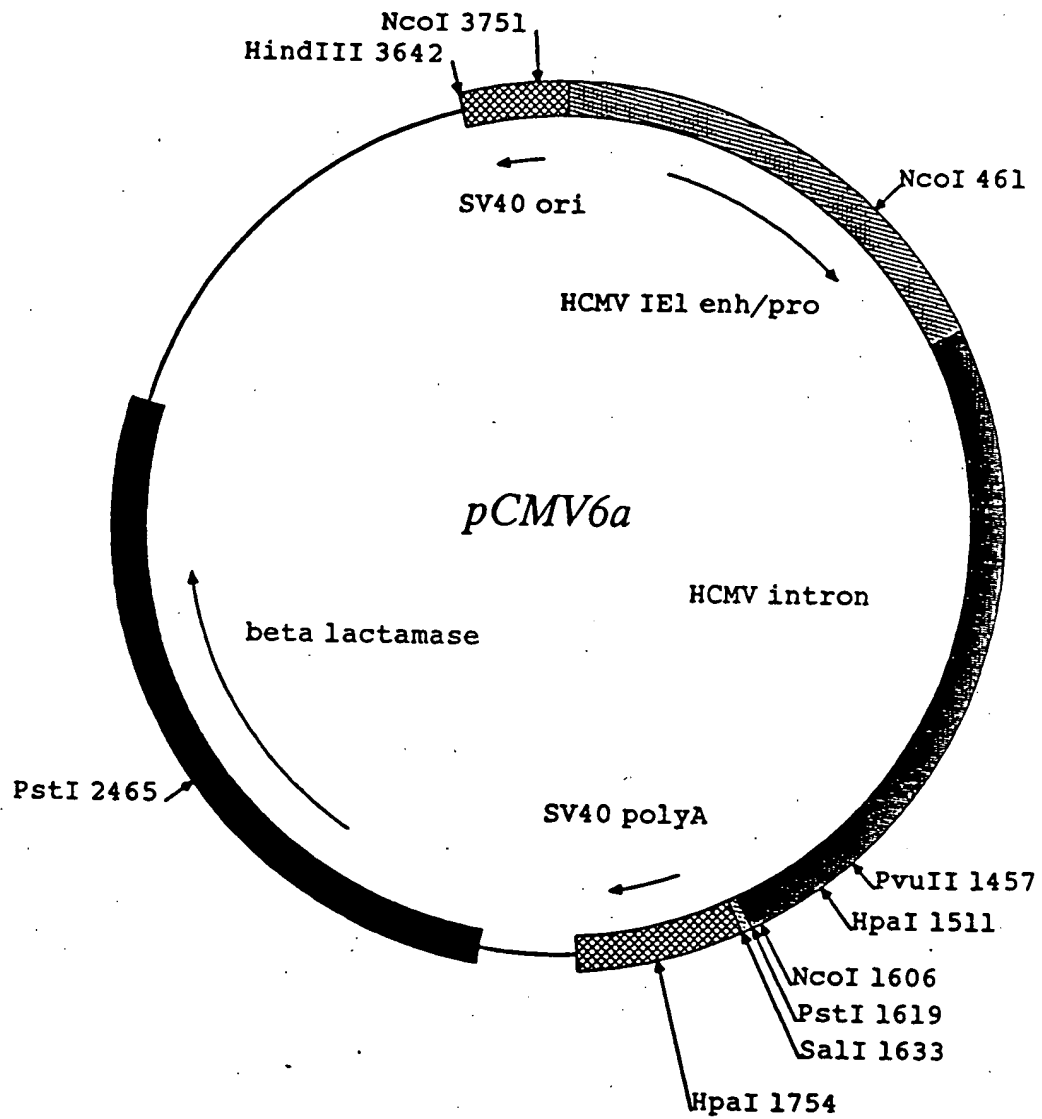


FIGURE 29

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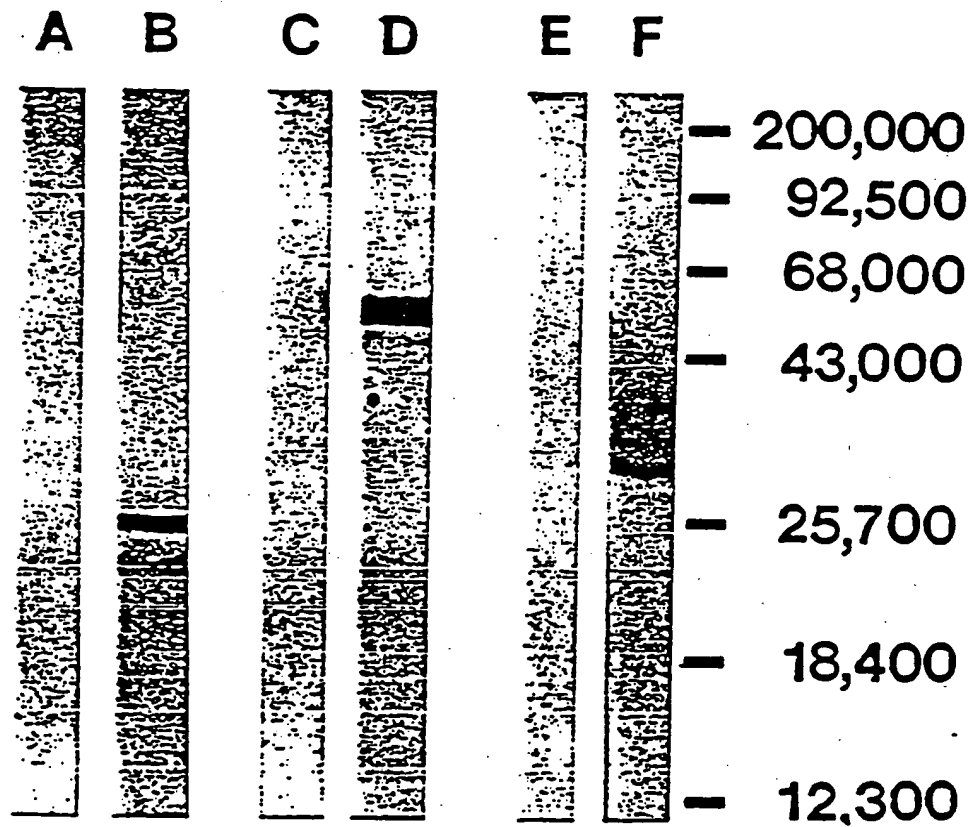


FIGURE 30